

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 15, 2001, 12:11:55 ; Search time 23.78 seconds
(without alignments)
1157.252 Million cell updates/sec

Title: US-09-284-100-2
Perfect score: 1125
Sequence: 1 MWKWLTHCASAPPHLPGCC.....GQTRKNTSAHFLPMVHS 208

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1046.5	93.0	213	6 Q9N1B9	Q9n1b9 ovis aries
2	932	82.8	212	13 Q42407	Q42407 gallus gall
3	473.5	42.1	194	6 P79150	P79150 canis fami
4	467.5	41.6	194	6 Q9N198	Q9n198 sus scrofa
5	441	39.2	170	4 Q9HCT0	Q9hct0 homo sapien
6	440.5	39.2	185	11 Q9ERN5	Q9ern5 rattus norv
7	437	38.8	162	11 Q9ESS2	Q9ess2 mus musculu
8	321	28.5	207	11 Q9ERQ5	Q9erq5 mus musculu
9	313	27.8	207	11 Q9ESL8	Q9esl8 mus musculu
10	309	27.5	129	4 Q60371	Q60371 mus musculu
11	308	27.4	211	4 Q9NFP5	Q9npf5 mus sapien
12	307.5	27.3	208	13 Q9PVI1	Q9pvi1 xenopus lae
13	305	27.1	212	11 Q9ESL9	Q9esl9 mus musculu
14	302	26.8	212	11 Q9EST9	Q9est9 rattus norv
15	281.5	25.0	97	4 Q9NSU0	Q9nsj0 mus sapien
16	257	22.8	243	13 Q9W6A1	Q9w6a1 gallus gall
17	256.5	22.8	191	13 Q9DFC9	Q9dfc9 brachydanio
18	254	22.6	245	13 Q9W6A2	Q9w6a2 gallus gall
19	251	22.3	192	11 Q9ERW3	Q9erw3 rattus norv

20	251	22.3	199	13 Q9IAI3	Q9iai3 gallus gall
21	248	22.0	192	4 Q95830	Q95830 homo sapien
22	245.5	21.8	196	13 Q9YH31	Q9yh31 notophthalm
23	244	21.7	181	13 Q9IAI7	Q9iai7 gallus gall
24	242.5	21.6	206	13 Q9YCD8	Q9ygd8 oncorhynch
25	242	21.5	127	4 Q99517	Q99517 homo sapien
26	238	21.2	73	6 Q97573	Q97573 sus scrofa
27	219.5	19.5	770	5 P91672	P91672 drosophila
28	219.5	19.5	770	5 Q9VDT9	Q9vdt9 drosophila
29	213.5	19.0	252	11 Q89096	Q89096 rattus norv
30	213.5	19.0	253	13 Q9IAI5	Q9iai5 gallus gall
31	212	18.8	237	13 Q9IAI6	Q9iai6 gallus gall
32	208	18.5	74	6 Q77561	Q77561 oryctolagus
33	203	18.0	130	6 Q77767	Q77767 canis fami
34	203	18.0	196	4 P78443	P78443 homo sapien
35	201	17.9	425	5 Q76831	Q76831 caenorhabdi
36	200	17.8	170	11 Q60487	Q60487 cavia porce
37	196	17.4	163	11 Q9JHL9	Q9jhl9 mus musculu
38	177	15.7	108	6 Q9N1S7	Q9n1s7 capreolus c
39	177	15.7	227	13 Q9DDN0	Q9ddn0 gallus gall
40	174	15.5	106	6 Q9N1S8	Q9n1s8 capreolus c
41	171	15.2	101	13 P79706	P79706 cynops pyrr
42	170.5	15.2	87	13 Q9PTV9	Q9ptv9 oryzias lat
43	170.5	15.2	87	13 Q9PTV8	Q9ptv8 oryzias lat
44	168	14.9	97	6 Q9NOK6	Q9nok6 sus scrofa
45	166	14.8	212	13 Q9DE51	Q9de51 ambystoma m

ALIGNMENTS

RESULT 1	
Q9N1B9	PRELIMINARY; PRT; 213 AA.
ID Q9N1B9	
AC Q9N1B9	
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE FIBROBLAST GROWTH FACTOR 10.	
GN FGF-10.	
OS Ovis aries (Sheep).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC Bovidae; Caprinae; Ovis.	
OX NCBI_TaxID=9940;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE-ENDOMETRIUM FROM DAY 15 PREGNANT UTERUS;	
RA Chen C., Spencer T.E., Bazer F.W.;	
RT "Fibroblast growth factor 10: a stromal mediator of epithelial	
RL function in the ovine uterus and conceptus.";	
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
DR EMBL: AF213396; AAF25944.1;	
DR InterPro: IPR002209;	
DR InterPro: IPR002348;	
DR Pfam: PF00167; FGF; 1.	
DR PRINTS; PR00263; HBGFFGF.	
DR PRINTS; PR00262; IL1HBGF.	
DR PROSITE; PS00247; HBGF_FGF; UNKNOWN1.	
DR SMART; SM00442; FGF; 1.	
SQ SEQUENCE 213 AA; 23768 MW; C347149A81C15634 CRC64;	

Query Match	93.0%;	Score 1046.5;	DB 6;	Length 213;
Best Local Similarity	94.0%;	Pred. No. 2.5e-87;		
Matches 202;	Conservative	0;	Mismatches 4;	Indels 9;
Gaps	3;			
QY 1	MWKWLTHCASAPPHLPGCCCFLLFLVSSVPVTCQALGQDMVSPEATNSSSSFS-	59		
Db 1	MWKWLTHCASAPPHLSG-CCCCFLLLFLVSSVPVTCQALDQDMVSPGATNSSSSSSSS	59		
QY 60	-----PSSAGRHVRSYHNLQGDVRRKLFSTKTKFLKIEKNGKVGKNCPCYSILEI	113		

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Db 60 SSSVSLPSAGRHVRSYHNHLOGDVRWKLFSPTKYFLKIE-NGKVGSTKKENCYPYSILEI 118
QY 114 TSVEIGVAVKAINSYYLAMNKKGLYSGKFEFNDCKLKERIEBNGYNTYASFNWQHG 173
Db 119 TSVEIGVAVKAINSYYLAMNKKGLYSGKFEFNDCKLKERIEBNGYNTYASFNWQHG 178
QY 174 ROMYVALNGKGAPRGOKTRRRKNTSAHFLPMVVHS 208
Db 179 ROMYVALNGKGAPRGOKTRRRKNTSAHFLPMVVHS 213

RESULT 2
O42407 PRELIMINARY; PRT; 212 AA.
AC O42407:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP MEDLINE=97330690; PubMed=9187149;
RA Ohuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
RA Yoshiohka H., Kuwana T., Nohno T., Yamasaki M., Itoh N., Noji S.;
RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
RT of the chick limb bud through interaction with FGF8, an apical
RT ectodermal factor."
RL Development 124:2235-2244 (1997).
DR EMBL; D86333; BAA24945.1; -
DR HSSP; P03968; IBAR.
DR InterPro; IPR002209; -
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR ProDom; PD000831; -; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;

Query Match 82.8%; Score 932; DB 13; Length 212;
Best Local Similarity 84.2%; Pred. No. 6e-77;
Matches 181; Conservative 12; Mismatches 12; Indels 10; Gaps 2;

QY 1 MWKWLTHCASAPFLPGCCCFILLFLVSSVPVTCQALGQDMVSPKATNSS----- 54
Db 1 MCKWILTNGASAFSLP---CCCLLLFLVSSVPVTCQALGQDMVSPKATNSSSSSSSF 57
QY 55 -SSFSPPSSAGRHVRSYHNHLOGDVRWKLFSFTKYFLKIEKNGKVGSTKKENCYPYSILEI 113
Db 58 PSFSPSSAGRHVRSYHNHLOGDVRWKLFSYNYKFLKIEKNGKVGSTKKENCYPYSILEI 117
QY 114 TSVEIGVAVKAINSYYLAMNKKGLYSGKFEFNDCKLKERIEBNGYNTYASFNWQHG 173
Db 118 TSVEIGVAVKAINSYYLAMNKKGLYSGKFEFNDCKLKERIEBNGYNTYASFNWQHG 177

QY 174 ROMYVALNGKGAPRGOKTRRRKNTSAHFLPMVVHS 208
Db 178 ROMYVALNGKGAPRGOKTRRRKNTSAHFLPMVVHS 212

RESULT 3
P79150 PRELIMINARY; PRT; 194 AA.
ID P79150:
AC P79150:
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KERATINOCYTE GROWTH FACTOR.
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226403; PubMed=8634153;
RA Canatan H., Chang W.Y., Sugimoto Y., Shidaifat F., Kulp S.K.,
RA Brueggemeier R.W., Lin Y.C.;
RT "Keratinocyte growth factor (KGF/FGF-7) has a paracrine role in canine
RT prostate: molecular cloning of mRNA encoding canine KGF.";
RL DNA Cell Biol. 15:247-254 (1996).
DR EMBL; U80800; AAB36972.1; -
DR HSSP; P05230; 2AFG.
DR InterPro; IPR002209; -
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; -; 1.
DR SMART; PS00247; HBGFFGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 194 AA; 22476 MW; 8B4E56304B8F14D6 CRC64;

Query Match 42.1%; Score 473.5; DB 6; Length 194;
Best Local Similarity 46.9%; Pred. No. 2e-35;
Matches 98; Conservative 38; Mismatches 54; Indels 19; Gaps 6;

QY 1 MWKWLTHCASAPFLPGCCCFILLFLVSSVPVTCQALGQDMVSPKATNSSSSSFS 58
Db 1 MRKWILTWPILTYLR-----SCFHIICLVGTISLAC-----NDM-TPEQMATVNC----- 46
QY 59 SPSSAGRHVRSYHNHLOGDVRWKLFSFTKYFLKIEKNGKVGSTKKENCYPYSILETSVE 117
Db 47 -SSPERHTRSYDYMGGDIRVRLFCRTOWYLRIDRKRGVKGTQEMKNSYNIETVA 104
QY 118 IGTVAVKAINSYYLAMNKKGLYSGKFEFNDCKLKERIEBNGYNTYASFNWQHGROMY 177
Db 105 VGVIAIKGVSESYLAMNKKGLYAKKEDCDNFLEILLENHYNYASAKWTHSGGEMF 164
QY 178 VALNGKGAPRGOKTRRRKNTSAHFLPMV 206
Db 165 VALNGKGVPRGKTKKREKTAHFLPMAI 193

RESULT 4
ID O9N198 PRELIMINARY; PRT; 194 AA.
AC O9N198:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KERATINOCYTE GROWTH FACTOR (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=12 DAYS POST-PREGNANCY ENDOMETRIUM;
RA Ka H., Spencer T.E., Bazer F.W.;
RT "Keratinocyte growth factor: expression by endometrial epithelia of
RT the porcine uterus";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217463; AAF26734.1; -
DR InterPro; IPR002209; -
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00263; HBGFFGF.
DR PRINTS; PR00262; IL1HBGF.
DR PROSITE; PS00247; HBGFFGF; 1.
DR SMART; SM00442; FGF; 1.
FT NON_TER 194

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SQ SEQUENCE 194 AA; 22463 MW; BA4495B45A731B0 CRC64;

Query Match
Best Local Similarity 41.6%; Score 467.5; DB 6; Length 194;
Matches 98; Conservative 38; Mismatches 54; Indels 19; Gaps 6;

QY 1 MKKWILTHCASFPHLPCCGCCCLLLFLVSSVPVTCOALGQDMVSP--ATNSSSSSFS 58
DB 1 MKKWILTHCASFPHLPCCGCCCLLLFLVSSVPVTCOALGQDMVSP--ATNSSSSSFS 58
QY 59 SPSSAGRHVRSYHNLQ-GDVRWRKLFSTKYFLKIEKNGKVSCTKENCPSYILEITSVEI 117
DB 47 --SPERHTRSDYMEGGDIRVRLFCRTOWYPRIGRGKVKGTQEMRNYSYINMEIRTV 104
QY 118 IGVAVKAINSYLLAMNKGKLYGSKFENNDCKLKERIEENGYNTYASFNWOHNGROMY 177
DB 105 GVAIVKAINSYLLAMNKGKLYGSKFENNDCKLKERIEENGYNTYASFNWOHNGROMY 177
QY 178 VALNGKAPRRGOKTRKNTSAHFLPMV 206
DB 165 VALNGKAPRRGOKTRKNTSAHFLPMV 193

RESULT 5
Q9HCT0 PRELIMINARY; PRT; 170 AA.
ID Q9HCT0
AC Q9HCT0
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF-22.
GN FGF22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "human FGF-22.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021925; BAB13479.1;
SQ SEQUENCE 170 AA; 19662 MW; CB88918C2D54ACE7 CRC64;

Query Match
Best Local Similarity 39.2%; Score 441; DB 4; Length 170;
Matches 81; Conservative 37; Mismatches 35; Indels 8; Gaps 1;

QY 46 SPATNSSSSSFSPPSSAGRHVRSYHNLQGDVRWRKLFSTKYFLKIEKNGKVSCTKKN 105
DB 17 APDAAGTPSAS-----RGPRSYPHLEGGDVRWRRLFSSTHFFLRVDPGGRVGTWR 68
QY 106 CPYSILEITSVEIGVAVKAINSYLLAMNKGKLYGSKFENNDCKLKERIEENGYNTYA 165
DB 69 QDSILEIRSVHGVVIVKAVSGEYVAMNRGLYSLYVDCRFRERIEENGHTYA 128
QY 166 SFNWOHNGROMYVALNGKAPRRGOKTRKNTSAHFLPMV 206
DB 129 SQWRRRGQPMFALDRGGRPRGGRTRKYHLSAHFLPLV 169

RESULT 6
Q9ERN5 PRELIMINARY; PRT; 185 AA.
ID Q9ERN5
AC Q9ERN5
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF7/KGF (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

us-09-284-100-2.rspt
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DARK AGUT1;
RA Choi J.K.W., Gibbins J.R., Hunter N., Lyons J.G., Tazawa M.Y.,
RA Walker D.M.;
RT "Novel CD44 Splice Variants Associated with Changes in Alternative
RT Splicing of FGF-2 and Expression of FGF-2, FGF-7, E-Cadherin and
RT Snail";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF295300; AAG31597.1;
FT NON_TER 185
SQ SEQUENCE 185 AA; 21340 MW; 8DBB364C9222B88 CRC64;

Query Match
Best Local Similarity 39.2%; Score 440.5; DB 11; Length 185;
Matches 95; Conservative 35; Mismatches 49; Indels 17; Gaps 7;

QY 1 MKKWILTHCASFPHLP-GCCCCCFLLLFLVSSVPVTCOALGQDMVSPATNSSSSSFS 59
DB 1 MKKWILTHCASFPHLP-GCCCCCFLLLFLVSSVPVTCOALGQDMVSPATNSSSSSFS 59
QY 60 SPSSAGRHVRSYHNLQ-GDVRWRKLFSTKYFLKIEKNGKVSCTKENCPSYILEITSVEI 118
DB 49 PE---RHTRSDYMEGGDIRVRLFCRTOWYPRIGRGKVKGTQEMRNYSYINMEIRTV 105
QY 119 GVAIVKAINSYLLAMNKGKLYGSKFENNDCKLKERIEENGYNTYASFNWOHNGROMY 178
DB 106 GVAIVKAINSYLLAMNKGKLYGSKFENNDCKLKERIEENGYNTYASFNWOHNGROMY 178
QY 179 ALNGKAPRRGOKTRR 194
DB 166 ALNGKAPRRGOKTRR 181

RESULT 7
Q9ESS2 PRELIMINARY; PRT; 162 AA.
ID Q9ESS2
AC Q9ESS2
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF-22.
GN FGF-22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "mouse FGF-22.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036765; BAB16407.1;
SQ SEQUENCE 162 AA; 18927 MW; 225E512F4E1BE29 CRC64;

Query Match
Best Local Similarity 38.8%; Score 437; DB 11; Length 162;
Matches 77; Conservative 35; Mismatches 34; Indels 4; Gaps 1;

QY 59 SPSSAGRHVRSYHNLQGDVRWRKLFSTKYFLKIEKNGKVSCTKENCPSYILEITSVEI 118
DB 17 APGAPG---GYPHLEGGDVRWRRLFSSTHFFLRVDPGGRVGTWRHRCODSIVEIRSV 72
QY 119 GVAIVKAINSYLLAMNKGKLYGSKFENNDCKLKERIEENGYNTYASFNWOHNGROMY 178
DB 73 GTWIKAVYSGFYVAMNRGLYSLYVDCRFRERIEENGHTYA 132
QY 179 ALNGKAPRRGOKTRRKNNTSAHFLPMV 208
DB 179 ALNGKAPRRGOKTRRKNNTSAHFLPMV 208
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Db 133 ALDSOGIPROGRRTRRHHQSTHFLPLVSS 162
RESULT 8
Q9ERO5 PRELIMINARY; PRT; 207 AA.
AC Q9ERO5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF-16 PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Sontag D.P., Cattini P.A.;
RT "Cloning and biological function of FGF-16 in the heart.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292104; AAG29501.1; --
SQ SEQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;

Query Match 28.5%; Score 321; DB 11; Length 207;
Best Local Similarity 34.6%; Pred. No. 1.4e-21;
Matches 71; Conservative 41; Mismatches 65; Indels 28; Gaps 4;

QY 4 WILTHCASFPHLPGCCCCFLLFLVSSVPTVCALQDMVSPDATNSSSSFSFSSA 63
Db 13 WDLQGFSSSLGNVP-----LADSPGFLNERLQO--IEGKLGSGPTDFA----- 54
QY 64 GRHVSYNHLOGDVRWRKLFSTKFKYFKTEKNGKYGSGTKKENCYPYSILEITSVEIGVAV 123
Db 55 -----HLKGLIRRRQLYCRTGFLEIFPNGTVHGRHDSRFGILEFISLAVGLISI 106
QY 124 KAINSNIYLAAMKKGKLYGSKFNNCKLKERIEENGYNTYASFNNQNG--RQMYVALN 181
Db 107 RGVDSGLYLMNBERGELYGSKLTRECVFQFEENWYNTYASTLYKXSDSERQYVALN 166
QY 182 GKAPRRGQKTRKNTSAHFLPMV 206
Db 167 KGSPREGYTKRKHQKFTFLPRPV 191

RESULT 9
Q9ESL8 PRELIMINARY; PRT; 207 AA.
AC Q9ESL8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 16.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Itch N.;
RA "Mus musculus mRNA for FGF-16 (FGF16).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049219; BAB16405.1; --
SQ SEQUENCE 207 AA; 23751 MW; 68BD03BEDAALD84E CRC64;

Query Match 27.8%; Score 313; DB 11; Length 207;
Best Local Similarity 34.1%; Pred. No. 7.6e-21;
Matches 70; Conservative 40; Mismatches 67; Indels 28; Gaps 4;

QY 4 WILTHCASFPHLPGCCCCFLLFLVSSVPTVCALQDMVSPDATNSSSSFSFSSA 63
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Db 13 WDLHGFSSSLGNVP-----LADSPGFLNERLQO--IEGKLGSGPTDFA----- 54
QY 64 GRHVSYNHLOGDVRWRKLFSTKFKYFKTEKNGKYGSGTKKENCYPYSILEITSVEIGVAV 123
Db 55 -----HLKGLIRRRQLYCRTGFLEIFPNGTVHGRHDSRFGILEFISLAVGLISI 106
QY 124 KAINSNIYLAAMKKGKLYGSKFNNCKLKERIEENGYNTYASF--FNWQHNGRQMYVALN 181
Db 107 RGVDSGLYLMNBERGELYGSKLTRECVFQFEENWYNTYASTLYKXSDSERQYVALN 166
QY 182 GKAPRRGQKTRKNTSAHFLPMV 206
Db 167 KGSPREGYTKRKHQKFTFLPRPV 191

RESULT 10
O60371 PRELIMINARY; PRT; 129 AA.
ID O60371;
AC O60371;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE R33683_2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Garhes J., Danganan L., Poundstone P.,
RA Christensen M., Georgescu A., Avilla J., Liu S., Attix C., Andreise T.,
RA Tranckheim M., Amico-Keller G., Coefficient J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004449; AAC06148.1; --
DR HSSP; P09038; IBFG.
DR InterPro; IPR002209; --
DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; --; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 129 AA; 14637 MW; AC6ECC4C9594108C CRC64;

Query Match 27.5%; Score 309; DB 4; Length 129;
Best Local Similarity 55.7%; Pred. No. 1e-20;
Matches 54; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

QY 110 ILEITSVEIGVAVKATNSNYLAAMKKGKLYGSKFNNCKLKERIEENGYNTYASFNW 169
Db 32 ILEIRSVHGVVVVKAIVSSGVFVAMNRRGLYGLRVDCFRFRERIEENGHTYASORW 91
QY 170 OHNGRQMYVALNGKAPRRGQKTRKNTSAHFLPMV 206
Db 92 RRGQPMFLALDRGGPRPGGTRRYHLHSAHFLPV 128

RESULT 11
Q9NP95 PRELIMINARY; PRT; 211 AA.
ID Q9NP95;
AC Q9NP95;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FGF-20 (FIBROBLAST GROWTH FACTOR 20) (FGF-20).
GN FGF-20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20374469; PubMed=10913340;
 RA Kikoshiki H., Sagara N., Saitoh T., Tanaka K., Sekihara H.,
 RA Shikawa K., Katoh M.,
 RT "Molecular cloning and characterization of human FGF-20 on chromosome
 RT 8p21.3-p22.3;
 RL Biochem. Biophys. Res. Commun. 274:337-343(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Itoh N.;
 RT "Human FGF-20";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB044277; BAB03633.1; -;
 DR EMBL; AB030648; BAB03530.1; -;
 DR InterPro; IPR002209; -;
 DR InterPro; IPR002348; -;
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00263; HGFPGF.
 DR PRINTS; PR00262; ILIHGFG.
 DR PROSITE; PS00247; HGF_FGF; 1.
 DR SMART; SM00442; FGF; 1.
 SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;

Query Match 27.4%; Score 308; DB 4; Length 211;
 Best Local Similarity 35.9%; Pred. No. 2.2e-20;
 Matches 65; Conservative 37; Mismatches 67; Indels 12; Gaps 2;
 QY 38 QALGDQVMS-----PEATNSSSSSSPSSAGRHVSYNHLOGDVRWRKLFSTFK 87
 Db 15 EGLCQVGSHELLPPAGERPLLGERSAERSARGGPGAAHLHLRLRRQLYCRGT 74
 QY 88 YFLKIEKNGKVSFGKPCYSILEITSVEIGVVAVKAINSYLAMNKKGLYGSKEFN 147
 Db 75 FHLQILPDGVSQGTROHSLFGLIFTSVAVGLVSGVINGVDSGLYLGNDKGLYGSKELT 134
 QY 148 NDCKLKERIEENGNTYASFNWQH--NGROMYVALNGKGPAPRGQKTRRKNNTSAHFPLMV 205
 Db 135 SECIFREQEENWYNTSSNYIYKHGDTGRFYFVALNKDGTTPDGAARSKRHKQKTFHLP 194
 QY 206 V 206
 Db 195 V 195

RESULT 12
 Q9PVI1 ID Q9PVI1 PRELIMINARY; PRT; 208 AA.
 AC Q9PVI1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE XFGF-20.
 GN XFGF-20.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99373151; PubMed=10441498;
 RA Koga C., Adati N., Nakata K., Mikoshiba K., Furuhashi Y., Sato S.,
 RA Tei H., Sakaki Y., Kurokawa T., Shikawa K., Yokoyama K.K.;
 RT "Characterization of a novel member of the FGF family, XFGF-20, in
 RT Xenopus laevis";
 RL Biochem. Biophys. Res. Commun. 261:756-765(1999).
 DR EMBL; AB012615; BAA83474.1; -;
 DR HSSP; P05230; 2AFG.
 DR InterPro; IPR002209; -;
 DR InterPro; IPR002348; -;

DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00263; HGFPGF.
 DR PRINTS; PR00262; ILIHGFG.
 DR PROSITE; PS00247; HGF_FGF; 1.
 DR SMART; SM00442; FGF; 1.
 SQ SEQUENCE 208 AA; 23438 MW; 268881D36E757D4D CRC64;
 Query Match 27.3%; Score 307.5; DB 13; Length 208;
 Best Local Similarity 40.1%; Pred. No. 2.4e-20;
 Matches 63; Conservative 36; Mismatches 49; Indels 9; Gaps 2;
 QY 52 SSSSSPSSAGRHVSYNHLOGDVRWRKLFSTFKYFLKIEKNGKVSFGKPCYSIL 111
 Db 43 SERLSAAPS-----DLSHLQILRRRLYCRGTGHLQILPDGNNVQGTRODHSRFGIL 95
 QY 112 EITSVEIGVVAVKAINSYLAMNKKGLYGSKEFNNDCKLKERIEENGNTYASFNWQH 171
 Db 96 EFTSVAIGLVSRGVDYGLYLGNDKGLYGSKELTSECIFREQEENWYNTSSNYLKH 155
 QY 172 --NGROMYVALNGKGPAPRGQKTRRKNNTSAHFPLMVV 206
 Db 156 GDGRRYFVALNKDGTTPDGAARSKRHKQKTFHLP 192

RESULT 13
 Q9ESL9 ID Q9ESL9 PRELIMINARY; PRT; 212 AA.
 AC Q9ESL9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR 20.
 GN FGF20.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Itoh N.;
 RT "Mus musculus mRNA for FGF-20(FGF20).";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB049218; BAB16406.1; -;
 SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;

Query Match 27.1%; Score 305; DB 11; Length 212;
 Best Local Similarity 42.3%; Pred. No. 4.2e-20;
 Matches 58; Conservative 34; Mismatches 43; Indels 2; Gaps 1;
 QY 72 HLQGDVRWRKLFSTFKYFLKIEKNGKVSFGKPCYSILEITSVEIGVVAVKAINSY 131
 Db 59 HLHGILRRRLYCRGTGHLQILPDGTVGTRODHSRFGILFISVAVGLVSRGVDGLY 118
 QY 132 LAMNKKGLYGSKEFNNDCKLKERIEENGNTYASFNWQH--NGROMYVALNGKGPAPRG 189
 Db 119 LGMNDKGLYGSKELTSECIFREQEENWYNTSSNYIYKHGNTGRFYFVALNKDGT 178
 QY 190 QKTRRKNNTSAHFPLMVV 206
 Db 179 ARSKRRQKTFHLP 195
 RESULT 14
 Q9EST9 ID Q9EST9 PRELIMINARY; PRT; 212 AA.
 AC Q9EST9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 GN FGF-20.

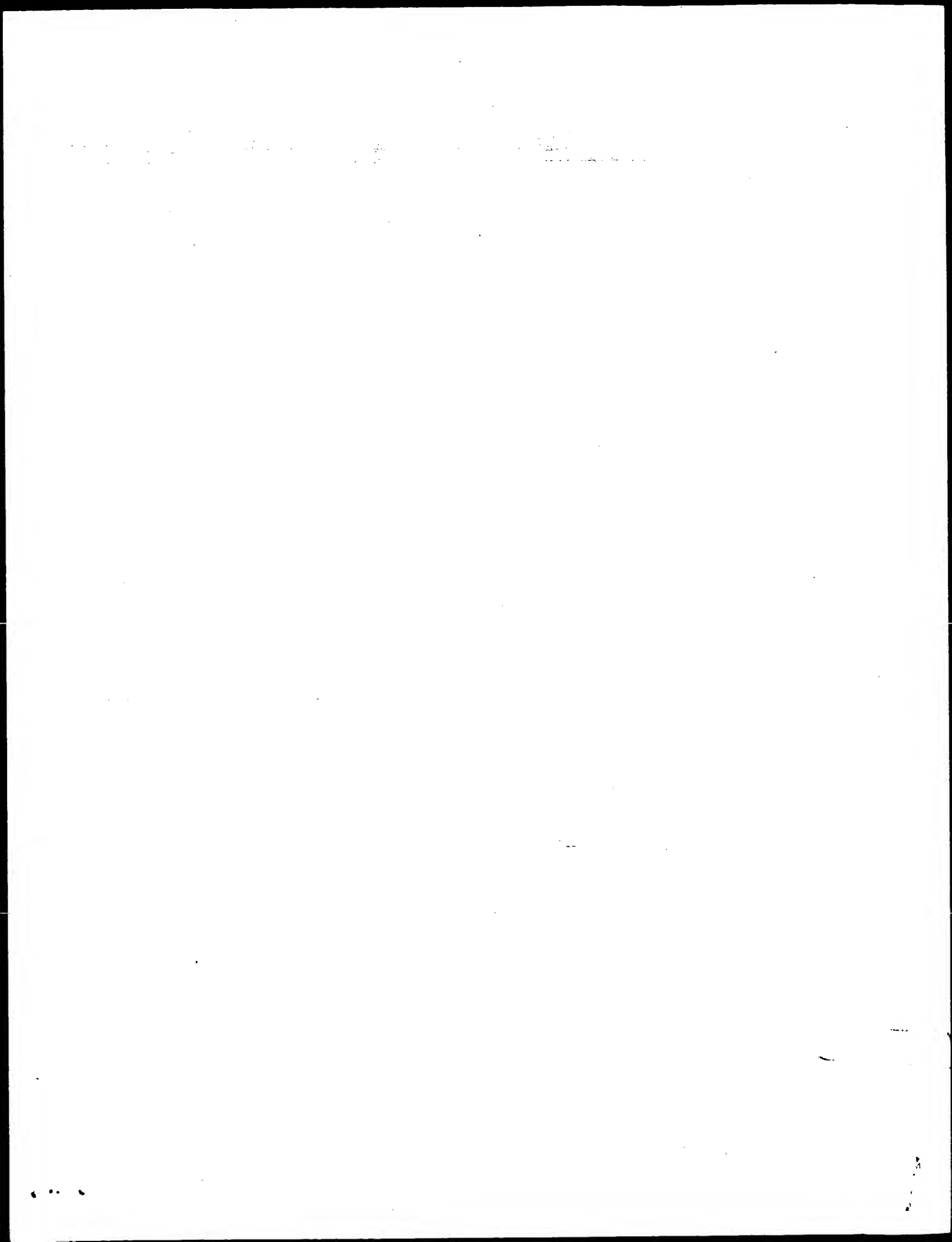
OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADULT BRAIN;
 RX PubMed=11032730;
 RA Ohnishi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
 RA Itoh N.;
 RT "FGF-20, a novel neurotrophic factor, preferentially expressed in the
 RT substantia nigra pars compacta of rat brain."
 RT Biochem. Biophys. Res. Commun. 277:355-360(2000).
 DR EMBL: AB020021; BAB13763.1;
 SQ SEQUENCE 212 AA; 23537 MW; 4F8508BEFE772B977 CRC64;

Query Match 26.8%; Score 302; DB 11; Length 212;
 Best Local Similarity 42.3%; Pred. No. 7.8e-20;
 Matches 58; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 72 HLOGDVRKLFSTFKYFLKTEKNCKYSGTKKENCYPYSILEITSVETGVAVKAINSNYY 131
 DB 59 HLHGTLRRQYCYRFGHLQILPDGSGVGTQDHSLSGLFISVAVGLVSIKGVDSGLY 118
 QY 132 LAMNKKGLYSGKEFNNDCKLKERIEENGYNFYASFNWQH--NGROMYVALNGKGPAPRG 189
 DB 119 LGMCKGELYSGEKLTSCEIFREQFEENWYNTSSNYKKGDTGRRYFVALNKDGTPRDG 178
 QY 190 QKTRRKNTSAHFLPMV 206
 DB 179 ARSKRHQKFTFLPRPV 195

RESULT 15
 QNSJO
 ID QNSJO PRELIMINARY; PRT; 97 AA.
 AC QNSJO;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE PRED3 PROTEIN (FRAGMENT).
 GN PRED3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.S.,
 RA Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E., Ohki M.,
 RA Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.L.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL163203; CAB90393.1;
 DR InterPro: IPR002209;
 DR InterPro: IPR002348;
 DR Pfam: PF00167; FGF; 1.
 DR PRINTS: PRO0263; HBGFFGF.
 DR PRINTS: PRO0262; ILIHGFG.
 DR SMART: SM00442; FGF; 1.
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10981 MW; 7D7AFFFF320C97E0 CRC64;

Query Match 25.0%; Score 281.5; DB 4; Length 97;
 Best Local Similarity 53.6%; Pred. No. 2.3e-18;
 Matches 52; Conservative 16; Mismatches 28; Indels 1; Gaps 1;
 QY 110 ILEITSVEIGVAVKAINSNYYLAMNKKGLYSGKEFNNDCKLKERIEENGYNFYASFNW 169
 DB 1 IMEIRTVAVGIVAIRGVESEFYLAMNEEGKLYAKKECNCNFKGLILENHYNTYASAKW 60
 QY 170 OHNGROMYVALNGKGPAPRGOKTRRKNTSAHFLPMV 206
 DB 61 THNGEMFVALNQKGPVR-KKNEERTKTAHFVPMAL 96
 Search completed: June 15, 2001, 12:13:36
 Job time: 101 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 15, 2001, 12:11:55 ; Search time 9.55 seconds
(without alignments)
746.088 Million cell updates/sec

Title: US-09-284-100-2

Perfect score: 1125

Sequence: 1 MKWILTHCASAPPLPGCC.....GQTRRKNTSAHFLPMVHVS 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1125	100.0	208	1 FGFA_HUMAN	O15520 homo sapien
2	1091.5	97.0	215	1 FGFA_RAT	P70492 rattus norv
3	1045.5	92.9	209	1 FGFA_MOUSE	O35565 mus musculu
4	481.5	42.8	194	1 FGF7_MOUSE	P36363 mus musculu
5	475.5	42.3	194	1 FGF7_SHEEP	P48808 ovis aries
6	473.5	42.1	194	1 FGF7_HUMAN	P21781 homo sapien
7	472.5	42.0	194	1 FGF7_RAT	Q02195 rattus norv
8	374	33.2	220	1 FGF3_CHICK	P48801 gallus gall
9	373	33.2	256	1 FGF3_BRARE	P48802 brachydanio
10	361	32.1	237	1 FGF3_XENLA	P36386 xenopus lae
11	353.5	31.4	245	1 FGF3_MOUSE	P05524 mus musculu
12	342.5	30.4	239	1 FGF3_HUMAN	P11487 homo sapien
13	328	29.2	208	1 FGF9_MOUSE	P31371 homo sapien
14	328	29.2	208	1 FGF9_HUMAN	P54130 mus musculu
15	328	29.2	208	1 FGF9_RAT	P36364 rattus norv
16	320	28.4	207	1 FGF9_HUMAN	O43320 homo sapien
17	317	28.2	207	1 FGF9_RAT	O54769 rattus norv
18	312	27.9	208	1 FGF5_XENLA	O91875 xenopus lae
19	291.5	25.9	268	1 FGF5_HUMAN	P12034 homo sapien
20	285.5	25.4	266	1 FGF5_MOUSE	P48807 rattus norv
21	282.5	25.1	264	1 FGF5_MOUSE	P15656 mus musculu
22	254	22.6	243	1 FGF5_HUMAN	O92912 homo sapien
23	253.5	22.5	187	1 FGF5_XENLA	P48805 xenopus lae
24	253	22.5	192	1 FGF5_MOUSE	P48806 xenopus lae
25	251	22.3	245	1 FGF5_HUMAN	P70377 mus musculu
26	248	22.0	245	1 FGF5_MOUSE	O92913 homo sapien
27	245.5	21.8	208	1 FGF5_HUMAN	P21658 mus musculu
28	244.5	21.7	208	1 FGF5_MOUSE	P10767 homo sapien
29	237.5	21.1	194	1 FGF5_CHICK	P48804 gallus gall
30	215	19.1	247	1 FGF5_HUMAN	O92915 homo sapien
31	214	19.0	247	1 FGF5_MOUSE	P70379 mus musculu
32	204	18.1	225	1 FGF5_HUMAN	O92914 homo sapien
33	203	18.0	154	1 FGF2_MOUSE	P15655 mus musculu

34	203	18.0	154	1 FGF2_RAT	P13109 rattus norv
35	203	18.0	155	1 FGF2_BOVIN	P03969 bos taurus
36	203	18.0	155	1 FGF2_HUMAN	P09038 homo sapien
37	203	18.0	155	1 FGF2_SHEEP	P20003 ovis aries
38	202	18.0	155	1 FGF1_HUMAN	P05230 homo sapien
39	201	17.9	225	1 FGF1_MOUSE	P70378 mus musculu
40	201	17.9	413	1 L756_MOUSE	Q11184 caenorhabdi
41	200	17.8	155	1 FGF1_MOUSE	P10935 mus musculu
42	198.5	17.6	206	1 FGF4_HUMAN	P08620 mus sapien
43	198	17.6	155	1 FGF1_MSAU	P34004 mesocricetu
44	198	17.6	156	1 FGF1_MONDO	P48798 monodelphis
45	197	17.5	155	1 FGF1_BOVIN	P03968 bos taurus

ALIGNMENTS

RESULT 1
FGFA_HUMAN
ID FGFA_HUMAN STANDARD; PRT; 208 AA.
AC O15520;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-10 PRECURSOR (FGF-10) (KERATINOCYTE GROWTH FACTOR 2).
DE FGF10.
GN FGF10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=97435285; PubMed=9287324;
RA Emoto H., Tagashira S., Mattei M.-G., Yamasaki M., Hashimoto G., Katsumata T., Negoro T., Nakatsuka M., Birnbaum D., Coulter F., Itoh N.;
RT "Structure and expression of human fibroblast growth factor-10.";
RL J. Biol. Chem. 272:23191-23194(1997).
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Jimenez P.A., Gruber J.R., Liu B., Peng P., Florence C., Blunt A., Huddleston K.A., Teliska M., Alfonso P., Coleman T.A., Ornitz D.M., Dillion P.A., Duan R.D.;
RT "Cutaneous wound healing by keratinocyte growth factor 2.";
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER SIMILAR TO FGF-7.
CC -!- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC EMBL; AB002097; BAA22331.1;
CC EMBL; U67918; AAB61991.1;
CC MIN; 602115;
DR InterPro; IPR002209;
DR InterPro; IPR002348;
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILLHGBF.
DR PRINTS; PR00263; HBGFFGF.
DR PROSITE; PS00247; HBGFFGF; 1.
KW Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 37 POTENTIAL.

	SIGNAL	1	36	POTENTIAL.
FT		37	215	FIBROBLAST GROWTH FACTOR-10.
FT	DOMAIN	51	69	POLY-SER.
FT	CARBOHYD	50	50	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	203	203	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQ	SEQUENCE	215 AA;	24029 MW;	93778EFA6FC0866A CRC64;

Query Match 97.0%; Score 1091.5; DB 1; Length 215;
Best Local Similarity 95.8%; Pred. No. 9.5e-91;
Matches 207; Conservative 0; Mismatches 0; Indels 9; Gaps 2;

Qy	1	MKWLLITHCASAFPHLPGCCCCCLLLLFLVSSVPVTQALGQDMVSPEATN-----S 52
Dd	1	MKWLLITHCASAFPHLP-G-CGCCFLLLFVSSVPVTQALGQDMVSPEATNSSSSSSS 59
Qy	53	SSSPSSPSSAGRHVRSYNHLOGDVWRKFLSFTKYFKLIEKKGVSTKKENCPSYLE 112
Dd	60	SSSPSSPSSAGRHVRSYNHQLQGVDWRKFLSFTKYFKLIEKKGVSGTKKENCPSYLE 119
Qy	113	ITSVELGVVAKAINSNLYLANMKKGKLYGSKEFNNDCKLERTEENGYNITYASFNMQHN 172
Dd	120	ITSVEIGVVAVKAINSNLYLANMKKGKLYGSKEFNNDCKLERTEENGYNITYASFNMQHN 179
Qy	173	GROMYVALNGKAPRRGQKTRKNKNTSAHFLPMVVHS 208
Dd	180	GROMYVALNGKAPRRGQKTRKNKNTSAHFLPMVVHS 215

PRT: 209 AA.

```

RESULT 3
FGFA_MOUSE STANDARD; PRT: 209 AA.
ID AC Q35365;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FIBROBLAST GROWTH FACTOR-10 PRECURSOR (FGF-10) (KERATINOCYTE GROWTH FACTOR 2).
DE MUS musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=97473538; PubMed=9332392;
RA Tagashira S., Harada H., Katsumata T., Itoh N., Nakatsuka M.;
RT "Cloning of mouse FGF10 and up-regulation of its gene expression during wound healing.";
RL Gene 197;399-404(1997).
RN [2]
RS SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Duan D.R., Florence C.;
PL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
CC -! FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER SIMILAR TO FGF-7.
CC -! SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -! TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN EMBRYOS AND THE LUNG, AND AT MUCH LOWER LEVELS IN BRAIN AND HEART.
CC -! SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC -----
DR EMBL; D89080; BAA2836.1; -
DR EMBL; U94517; AAD00761.1; -

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DR MGD; MGI:1099809; Fgf10.
 DR InterPro: IPR002209; -
 DR InterPro: IPR002348; -
 DR Pfam: PF00167; FGF, 1.
 DR PRINTS: PR00262; ILIHGFG.
 DR PRINTS: PR00263; HBGFFGF.
 DR PROSITE: PS00247; HBGFFGF, 1.
 KW Growth factor; Glycoprotein; Signal.
 FT SIGNAL 1 36
 FT CHAIN 37 209 FIBROBLAST GROWTH FACTOR-10.
 FT DOMAIN 52 63 POLY-SER.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 209 AA; 23597 MW; 7FD22227BF4943CC CRC64;

Query Match 92.9%; Score 1045.5; DB 1; Length 209;
 Best Local Similarity 93.3%; Pred. No. 1.2e-86;
 Matches 196; Conservative 5; Mismatches 6; Indels 3; Gaps 2;

QY 1 MKWILTHCASAFPHLPGCCGCCFLLFLVSSVPVTCQALGQDMVSPVATN--SSSSSFS 58
 Db 1 MKWILTHCASAFPHLPG--CCGCCFLLFLVSSVPVTCQALGQDMVSOEATNCSSSSSFS 59
 QY 59 SPSSAGRHVRSYHNLQGDVWRKLFSTKYFLKIEKNGKVSCTKNCPCYSILEITSVEI 118
 Db 60 SPSSAGRHVRSYHNLQGDVWRKLFSTKYFLKIEKNGKVSCTKNCPCYSILEITSVEI 119
 QY 119 GVAVKAINSYYLAMNKGKLYGSKFEFNNDCKLKERIEENGYNVYASFNWONGROMYV 178
 Db 120 GVAVKAINSYYLAMNKGKLYGSKFEFNNDCKLKERIEENGYNVYASFNWONGROMYV 179
 QY 179 ALNGKAPRGOKTRRKNTSAHFLPMVVS 208
 Db 180 ALNGKAPRGOKTRRKNTSAHFLPMVVS 209

RESULT 4
 ID FGF7_MOUSE STANDARD; PRT; 194 AA.
 AC P36363;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (FGF-7) (HBGF-7).
 DE 7) (FGF-7) (HBGF-7).
 GN FGF7 OR FGF-7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94242659; PubMed=8186145;
 RA Mason I.J., Fuller-Pace F., Smith R., Dickson C.;
 RT "FGF-7 (keratinocyte growth factor) expression during mouse
 RT development suggests roles in myogenesis, forebrain regionalisation
 RT and epithelial-mesenchymal interactions.";
 RL Mech. Dev. 45:15-30(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N;
 RA Jones M.L., Dato M.E., Greenberg J.M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE
 CC MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; 222703; CAA80403.1; -
 DR EMBL; U58503; AAB01343.1; -
 DR PIR; S33227; S33227.
 DR HSSP; P09038; 2BFH.
 DR MGD; MGI:195521; Fgf7.
 DR InterPro: IPR002209; -
 DR InterPro: IPR002348; -
 DR Pfam: PF00167; FGF, 1.
 DR PRINTS: PR00262; ILIHGFG.
 DR PRINTS: PR00263; HBGFFGF.
 DR PROSITE: PS00247; HBGFFGF, 1.
 KW Growth factor; Mitogen; Signal.
 FT SIGNAL 1 31 BY SIMILARITY.
 FT CHAIN 32 194 KERATINOCYTE GROWTH FACTOR.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 194 AA; 22347 MW; 805C30D4B1D27C73 CRC64;

Query Match 42.8%; Score 481.5; DB 1; Length 194;
 Best Local Similarity 47.8%; Pred. No. 3.2e-36;
 Matches 99; Conservative 39; Mismatches 54; Indels 15; Gaps 6;

QY 1 MKWILTHCASAFPHLPGCCGCCFLLFLVSSVPVTCQALGQDMVSPVATNCSSSSFS 60
 Db 1 MKWILTRILPTLLYR-----SCFHLVCLVGTISLAC-----NDM-SPEQT-ATSVNCSSP 49
 QY 61 SSAGRHVRSYHNLQ--GDVWRKLFSTKYFLKIEKNGKVSCTKNCPCYSILEITSVEIG 119
 Db 50 E---RHTRSYDYMEGDIRVRRFLFCRTQWLRIDRKRGKVGTOEMKNSYNIETVAVG 106
 QY 120 VVAVKAINSYYLAMNKGKLYGSKFEFNNDCKLKERIEENGYNVYASFNWONGROMYVA 179
 Db 107 IVAIKGESEYLLAMNKGKLYAKKEDCNFKELILENHNTYASAKWTHSGGEMFA 166
 QY 180 LNKGAPRGOKTRRKNTSAHFLPMVVS 206
 Db 167 LNKGAPRGOKTRRKNTSAHFLPMVVS 193

RESULT 5
 ID FGF7_SHEEP STANDARD; PRT; 194 AA.
 AC P48808;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (FGF-7) (HBGF-7).
 DE 7) (FGF-7) (HBGF-7).
 GN FGF7 OR FGF-7.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mitchell J.E.A., McInnes C.J.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE
 CC MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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EMBL; Z46236; CAA86306.1; -
 DR HSP; P05230; 2AFG.
 DR InterPro; IPR002209; -
 DR InterPro; IPR002348; -
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; ILHGF.
 DR PRINTS; PR00263; HGF.
 DR PROSITE; PS00247; HGF_FGF; 1.
 DR Growth factor; Mitogen; Signal.
 KW SIGNAL 1 31 BY SIMILARITY.
 FT CHAIN 32 194 KERATINOCYTE GROWTH FACTOR.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 194 AA; 22448 MW; 80F4F4BC5B76F668 CRC64;

Query Match 42.3%; Score 475.5; DB 1; Length 194;
 Best Local Similarity 47.6%; Pred. No. 1.1e-35;
 Matches 100; Conservative 37; Mismatches 52; Indels 21; Gaps 7;
 QY 1 MKRWILTHCASFPHLPGCC-CCFLLLFLVSSVPVTCQALGQDMVSP--ATNSSSSSF 57
 Db 1 MKRWILTWI-----LPSLLYRSCFHIICLVGTISLAC-----NDM-TPEQMATVNC--- 46
 QY 58 SPSSAGRHVRSYNHLQ-GDVRWRKLFSTFKYFLKIEKNGKVSCTKKENCYPYSILEITSV 116
 Db 47 ---SSPERHTRSDYMEGGDIRVRLFCRTQWYLRIDKRGKVGKTOEMKNYINMEIRTV 103
 QY 117 EIGVAVKAINSYNYLAMNKKGLYKSEFNNDCKLKERIEENGYNYTASFVWQHNGROM 176
 Db 104 AVGIVAIGVESEYNYLAMNKKGLYKSEFNNDCKLKERIEENGYNYTASFVWQHNGROM 163
 QY 177 YVALNGKAPRRGOKTRKNTSAHFLPMV 206
 Db 164 FVALNSKGVPRGKTKKOKTAHFLPM 193

RESULT 6
 FGF7_HUMAN
 ID FGF7_HUMAN STANDARD; PRT; 194 AA.
 AC P21781;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (FGF-7) (HBGF-7).
 DE FGF7 OR KGF.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-50.
 RX MEDLINE=89368897; PubMed=2475908;
 RA Finch P.W., Rubin J.S., Miki T., Ron D., Aaronson S.A.;
 RT "Human KGF is FGF-related with properties of a paracrine effector of epithelial cell growth."
 RL Science 245:752-755(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92152720; PubMed=1664700;
 RA Aaronson S.A., Bottaro D.P., Miki T., Ron D., Finch P.W.,
 RA Fleming T.P., Ahn J., Taylor W.G., Rubin J.S.;
 RT "Keratinocyte growth factor. A fibroblast growth factor family member with unusual target cell specificity."
 RL Ann. N.Y. Acad. Sci. 638:62-77(1991).
 RN [3]
 RP SEQUENCE OF 32-44.
 RX MEDLINE=89128865; PubMed=2915979;
 RA Rubin J.S., Osada H., Finch P.W., Taylor W.G., Rudikoff S.,
 RA Aaronson S.A.;
 RT "Purification and characterization of a newly identified growth factor specific for epithelial cells."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:802-806(1989).

CC -1- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE
 CC MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION.
 CC -1- TISSUE SPECIFICITY: EPITHELIAL CELL.
 CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC -----
 DR EMBL; M60828; AAA63210.1; -
 DR EMBL; S81661; AAB21431.1; -
 DR PIR; A31453; A31453.
 DR PIR; A36301; A36301.
 DR HSP; P05230; 2AFG.
 DR MIN; 148180; -
 DR InterPro; IPR002209; -
 DR InterPro; IPR002348; -
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; ILHGF.
 DR PRINTS; PR00263; HGF_FGF.
 DR PROSITE; PS00247; HGF_FGF; 1.
 DR Growth factor; Mitogen; Signal.
 KW SIGNAL 1 31
 FT CHAIN 32 194 KERATINOCYTE GROWTH FACTOR.
 FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 194 AA; 22509 MW; B19192474E6049E2 CRC64;

Query Match 42.1%; Score 473.5; DB 1; Length 194;
 Best Local Similarity 46.9%; Pred. No. 1.1e-35;
 Matches 98; Conservative 38; Mismatches 54; Indels 19; Gaps 6;
 QY 1 MKRWILTHCASFPHLPGCC-CCFLLLFLVSSVPVTCQALGQDMVSP--ATNSSSSSF 58
 Db 1 MKRWILTWIPLTYR-----SCFHIICLVGTISLAC-----NDM-TPEQMATVNC--- 46
 QY 59 SPSSAGRHVRSYNHLQ-GDVRWRKLFSTFKYFLKIEKNGKVSCTKKENCYPYSILEITSV 117
 Db 47 ---SSPERHTRSDYMEGGDIRVRLFCRTQWYLRIDKRGKVGKTOEMKNYINMEIRTV 104
 QY 118 IGVAVKAINSYNYLAMNKKGLYKSEFNNDCKLKERIEENGYNYTASFVWQHNGROM 177
 Db 105 VGIVAIGVESEYNYLAMNKKGLYKSEFNNDCKLKERIEENGYNYTASFVWQHNGROM 164
 QY 178 YVALNGKAPRRGOKTRKNTSAHFLPMV 206
 Db 165 VALNQKGVPRGKTKKOKTAHFLPM 193

RESULT 7
 FGF7_RAT
 ID FGF7_RAT STANDARD; PRT; 194 AA.
 AC Q02195;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE KERATINOCYTE GROWTH FACTOR PRECURSOR (KGF) (FIBROBLAST GROWTH FACTOR-7) (FGF-7) (HBGF-7).
 DE FGF7 OR FGF-7 OR KGF.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9133191; PubMed=1869483;
 RA Yan G., Nikolopoulos S., Wang F., McKeehan W.L.;
 RT "Sequence of rat keratinocyte growth factor (heparin-binding growth factor type 7).";

In Vitro Cell. Dev. Biol. 27A:437-438(1991).

-!- FUNCTION: GROWTH FACTOR ACTIVE ON KERATINOCYTES. POSSIBLE MAJOR PARACRINE EFFECTOR OF NORMAL EPITHELIAL CELL PROLIFERATION.

-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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EMBL; X56551; CAA39892.1; -
 HSP; P09038; 2BPH.
 InterPro; IPR002209; -
 InterPro; IPR002348; -
 Pfam; PF00167; FGF; 1.
 PRINTS; PR00262; ILLHGF.
 PROSITE; PS00263; HGGFFG.
 PROSITE; PS00247; HBGF_FGF; 1.
 Growth factor; Mitogen; Signal.
 SIGNAL 1 31 BY SIMILARITY.
 CHAIN 32 194 KERATINOCYTE GROWTH FACTOR.
 CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 194 AA; 22268 MW; 5242CDAC305CC8C1 CRC64;

Query Match 42.08; Score 472.5; DB 1; Length 194;
 Best Local Similarity 47.3%; Pred. No. 2e-35;
 Matches 98; Conservative 40; Mismatches 54; Indels 15; Gaps 6;

QY 1 MKWILTHCASAFPHLPCCGCCGELLFLVSYVPVTCQALQDMVSPKATNSSSSFSSP 60
 DB 1 MKWILTRILPTLYRP-----CFHLVCLVGTISLAC-----NDM-SPEQT-ATSVNCSPP 49

QY 61 SSAGRHRSYNHLO-GDVRWRKLFSTFKYPLKTEKNGKVGTKKENCPCYSILEITSVEIG 119
 DB 50 E---RHTRSVDYMEGGDIRVRLFCRTQWYLRIDKRGKVGQEMKNSNIMEIMTVAVG 106

QY 120 VVAVKATNSNYLLAMNKKGLYSGKFNNDCKLKERIENGNTYASFNWQHNGRMQYVA 179
 DB 107 IVAIKGVSEYLLAMNKKGLYAKKEDCNFCNELILENHNTSASAKWTHSGGEMFVA 166

QY 180 LNKGAPRRGQKTRRKNTSAHFLPMV 206
 DB 167 LNKGLPVKCKTKKQKTAHFLPM 193

RESULT 8
 FGF3_CHICK
 ID FGF3_CHICK STANDARD; PRT; 220 AA.
 AC P48801;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR-3 PRECURSOR (FGF-3) (HBGF-3).
 GN FGF3 OR FGF-3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RHODE ISLAND RED; TISSUE=Embryo;
 RX MEDLINE=95309122; PubMed=7789270;
 RA Mahmood R., Kiefer P., Guthrie S., Dickson C., Mason I.;
 RT "Multiple roles for FGF-3 during cranial neural development in the chicken."
 RL Development 121:1399-1410(1995).
 CC -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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EMBL; Z47555; CAA87635.1; -
 HSP; P09038; 1BFC.
 InterPro; IPR002209; -
 InterPro; IPR002348; -
 Pfam; PF00167; FGF; 1.
 PRINTS; PR00262; ILLHGF.
 PROSITE; PS00263; HGGFFG.
 PROSITE; PS00247; HBGF_FGF; 1.
 Growth factor; Mitogen; Signal; Glycoprotein.
 SIGNAL 1 220 POTENTIAL.
 CHAIN 66 66 FIBROBLAST GROWTH FACTOR-3.
 CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 220 AA; 25050 MW; B15D41DIE55IC5D5 CRC64;

Query Match 33.2%; Score 374; DB 1; Length 220;
 Best Local Similarity 46.7%; Pred. No. 1.5e-26;
 Matches 79; Conservative 30; Mismatches 48; Indels 12; Gaps 2;

QY 52 SSSSFSPSSAGRHRSYNHLOGDVNRKLFSTFKYPLKTEKNGKVGTKKENCPCYSIL 111
 DB 19 AATASPRAPRDAGGCVGVEHGLGAPRRRLKLYCATKYHLQHPGGKINGTLEKNSVFSIL 78

QY 112 EITSVEIGVAVKATNSNYLLAMNKKGLYSGKFNNDCKLKERIENGNTYAS--FMW 169
 DB 79 EITAVDVGIVAKLFSGRYLANKRGLYASENYTECEFEVERHELGYNSRLYRT 138

QY 170 QHNG-----ROMYVALNGKAPRRGQKTRRKNTSAHFLPMV 208
 DB 139 VPSCASTKPKASAEERLWYVSVNGKGRPRGRGKTRRTQKSSFLPRVLDS 187

RESULT 9
 FGF3_BRARE
 ID FGF3_BRARE STANDARD; PRT; 256 AA.
 AC P48802;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE FIBROBLAST GROWTH FACTOR-3 PRECURSOR (FGF-3) (HBGF-3).
 GN FGF3 OR FGF-3.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96204005; PubMed=8622866;
 RA Kiefer P., Strahle U., Mason I., Dickson C.;
 RT "Secretion and mitogenic activity of zebrafish FGF3 reveal intermediate properties relative to mouse and Xenopus homologues."
 RL Oncogene 12:1503-1511(1996).
 CC -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

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CC      ENBL; Z48714; CAA88596.1;
DR      HSSP; P09038; 2BFH
DR      ZFIN; ZDB-GENE-980526-178; fgf3.
DR      InterPro; IPR002209;
DR      InterPro; IPR002348;
DR      Pfam; PF00167; FGF; 1.
DR      PRINTS; PR00262; ILLHGF.
DR      PRINTS; PR00263; HGFPGF.
DR      PROSITE; PS00247; HBGF_FGF; 1.
KW      Growth factor; Mitogen; Signal; Glycoprotein.
FT      SIGNAL 1 ?
FT      CHAIN ? 256
SQ      SEQUENCE 256 AA; 28923 MW; CEBALC72A170BDBC CRC64;

Query Match 33.2%; Score 373; DB 1; Length 256;
Best Local Similarity 40.8%; Pred. No. 2,3e-26;
Matches 86; Conservative 34; Mismatches 55; Indels 36; Gaps 4;

QY      25 LLLFLVSVPTCOALGDMVSPATSSSSSFSSPSS-----AGHRVRSYNHLQGD 76
DB      5 LLLLLLFLDPSL---EESLAPRLTRPACARGACDPRQRDAGRGVYEHLGGA 60

QY      77 VWRKRLSFYFKLIKIKNGKSVSTKKNCPYSILEITSVEIGVAVKAINSXYLAMNK 136
DB      61 PRRRRLKCATYHLQIHFNKIDGSLSENNPLSILEITAVDVGVAIKGLFSRYLAMNE 120

QY      137 KGKLYGKEFNNDCKLERIEENYNIVYASFNMQHG-----RQ 175
DB      121 KGLRYASVFVNRCEFLERHELGINIYAS--RHATTQPTPGSIGGSKRRASSKRQ 177

QY      176 MYVALNGKAPRGQRQKTRKNTSAHFLPMVV 205
DB      178 WTVSYNGRGRPRGRGFKTRSTDKASLFLPRVL 208

RESULT 10
FGF3_XENLA
ID      FGF3_XENLA STANDARD; PRT; 237 AA.
AC      P36386;
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      FIBROBLAST GROWTH FACTOR-3 PRECURSOR (FGF-3) (HBGF-3) (INT-2).
GN      FGF3.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipelidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX      MEDLINE=94038898; PubMed=8223431;
RA      Kieffer P., Mathieu M., Close J.M., Peters G., Dickson C.;
RT      "FGF3 from Xenopus laevis.";
RL      EMBO J. 12:4159-4168(1993).
RN      [2]
RP      SEQUENCE OF 39-137 FROM N.A.
RC      TISSUE=Neurula;
RX      MEDLINE=93048831; PubMed=1425349;
RA      Tannahill D., Isaacs H.V., Close M.J., Peters G., Slack J.M.W.;
RT      "Developmental expression of the Xenopus int-2 (FGF-3) gene:
RT      activation by mesodermal and neural induction.";
RL      Development 115:695-702(1992).
CC      -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT.
CC      -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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RX MEDLINE-91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
RA Walther W., Fuller-Pace F., Kiefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor
RT family.";
RL J. Cell Sci. Suppl. 13:87-96(1990).
CC - FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC - INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC - SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC
DR EMBL; Y00846; CAA68767.1; -
DR PIR; A23930; TVMS22.
DR HSSP; P09038; 2BFH.
DR MGI; 95517; Fgf3.
DR InterPro; IPR002209; -
DR InterPro; IPR002348; -
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PROSITE; PS00263; HEGFFGF.
DR TRANSFORMING PROTEIN; Oncogene; Growth factor; Mitogen; Signal;
KW Glycoprotein. 1 17
FT SIGNAL 1 17
FT CHAIN 18 245
FT CARBOHYD 65 65
FT SEQUENCE 245 AA; 27214 MW; 70D94FD6A7837C79 CRC64;
Query Match 31.4%; Score 353.5; DB 1; Length 245;
Best Local Similarity 50.0%; Pred. No. 1.2e-24;
Matches 78; Conservative 22; Mismatches 43; Indels 13; Gaps 3;
QY 63 AGRHVSYNHLOGDVRWRKLFSTFYFLKIEKNGKVSSTKENCPCYSILEITSVEIGVVA 122
DB 29 AGRGGVYEHGGAPRRKLYCATKYHLQHPGSRVNGS-LENSAYSILEITAVEGVVA 87
QY 123 VKAINSNTYLANMKKGLYSGKEFNNDCKLKERIEENGYNTYAS--FNQHGNG----- 173
DB 88 IGLFSGRYLANMKRGLYASDHYNAECFEVERIHELGYNTYASRLYRTGSSGCPAQROP 147
QY 174 ---ROMYVALNGKAPRRGOKTRKNTSAHFLPMV 206
DB 148 GAQRWYVSVNGKGRPRGRGFKTRTQKSSLFPLRV 183
RESULT 12
FGF3_HUMAN
ID FGF3_HUMAN STANDARD; PRT; 239 AA.
AC P11487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INT-2 PROTO-ONCOGENE PROTEIN PRECURSOR (FIBROBLAST GROWTH FACTOR-3)
DE (FGF-3) (HBGF-3).
GN FGF3 OR INT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA MEDLINE-89239468; PubMed-2470007;
RX Brooks S., Smith R., Casey G., Dickson C., Peters G.;
RT "Sequence organization of the human int-2 gene and its expression in

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teratocarcinoma cells.";
OncoGene 4:429-436(1989).
- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
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DR EMBL; X14445; CAA32615.1; -
DR PIR; S04742; S04742.
DR HSSP; P09038; 2BFH.
DR MIM; 164950; -
DR InterPro; IPR002209; -
DR InterPro; IPR002348; -
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PROSITE; PS00263; HEGFFGF.
DR PROSITE; PS00247; HBGF_FGF_1.
KW Transforming protein; Oncogene; Growth factor; Mitogen; Signal;
KW Glycoprotein. 1 17
FT SIGNAL 1 17
FT CHAIN 18 239
FT CARBOHYD 65 65
FT SEQUENCE 239 AA; 26886 MW; 8DBEF17D2B2E3C63 CRC64;
Query Match 30.4%; Score 342.5; DB 1; Length 239;
Best Local Similarity 47.4%; Pred. No. 1.1e-23;
Matches 74; Conservative 26; Mismatches 43; Indels 13; Gaps 2;
QY 63 AGRHVSYNHLOGDVRWRKLFSTFYFLKIEKNGKVSSTKENCPCYSILEITSVEIGVVA 122
DB 29 AGRGGVYEHGGAPRRKLYCATKYHLQHPGSRVNGS-LENSAYSILEITAVEGVVA 87
QY 123 VKAINSNTYLANMKKGLYSGKEFNNDCKLKERIEENGYNTYASFNW----- 170
DB 88 IGLFSGRYLANMKRGLYASDHYNAECFEVERIHELGYNTYASRLYRTVSTSTPGARQP 147
QY 171 HNGROMYVALNGKAPRRGOKTRKNTSAHFLPMV 206
DB 148 SAERLWYVSVNGKGRPRGRGFKTRTQKSSLFPLRV 183
RESULT 13
FGF9_HUMAN
ID FGF9_HUMAN STANDARD; PRT; 208 AA.
AC P31371;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GLTA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9)
DE (FGF-9) (HBGF-9).
GN FGF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Foreskin;
RA MEDLINE-93309459; PubMed-8321227;
RX Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property.";
RL Mol. Cell. Biol. 13:4251-4259(1993).
RN [2]

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SEQUENCE Z06 AA; Z3413 MW; 4A3CE894DFF643EB CRC64;

Search completed: June 15, 2001, 12:13:08
Job time: 73 sec

us-09-284-100-2.rsp

Fri Jun 15 12:17:12 2001

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 15, 2001, 12:11:55 ; Search time 16.91 seconds
(without alignments)
936.979 Million cell updates/sec

Title: US-09-284-100-2
Perfect score: 1125
Sequence: 1 MWKWLTHCASAPPHLPGCC.....GQKTRKNTSAHFLPMVVS 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.68:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481.5	42.8	194	2 I48610	keratinocyte growth
2	475.5	42.3	194	2 S49501	keratinocyte growth
3	474.5	42.2	194	2 S26049	fibroblast growth
4	473.5	42.1	194	1 A36301	fibroblast growth
5	374	33.2	220	2 I50588	fibroblast growth
6	373	33.2	256	2 JC4627	fibroblast growth
7	361	32.1	237	1 S39582	transforming prote
8	353.5	31.4	245	1 TVM572	transforming prote
9	342.5	30.4	239	1 S04742	fibroblast growth
10	328	29.2	208	2 S66486	fibroblast growth
11	328	29.2	208	2 A48137	fibroblast growth
12	320	28.4	207	2 JC5941	fibroblast growth
13	317	28.2	207	2 JC5940	fibroblast growth
14	308	27.4	211	2 JC7353	fibroblast growth
15	307.5	27.3	208	2 JC7082	fibroblast growth
16	302	26.8	212	3 JC7511	fibroblast growth
17	301	26.8	98	2 B46289	fibroblast growth
18	297	26.4	98	2 C46289	keratinocyte growth
19	291	25.9	267	1 TVHUF5	fibroblast growth
20	285.5	25.4	266	2 S68144	fibroblast growth
21	282.5	25.1	264	2 A36207	fibroblast growth
22	269	23.9	96	2 D46289	fibroblast growth
23	253.5	22.5	187	2 S23595	embryonic fibrobla
24	253	22.5	192	2 S54407	embryonic fibrobla
25	245.5	21.8	208	2 S14192	fibroblast growth
26	244.5	21.7	208	2 S20102	fibroblast growth
27	239	21.2	168	2 JG0184	fibroblast growth
28	237.5	21.1	194	2 I50710	fibroblast growth
29	203	18.0	146	1 S00185	basic fibroblast g

30	203	18.0	154	2 A31674	basic fibroblast g
31	203	18.0	154	2 C37360	basic fibroblast g
32	203	18.0	157	1 GKBOH	basic fibroblast g
33	203	18.0	210	2 A32398	acidic fibroblast
34	202	18.0	155	1 A33665	acidic fibroblast
35	200	17.8	155	2 S04147	acidic fibroblast
36	200	17.8	155	2 D37360	acidic fibroblast
37	198.5	17.6	206	1 TVHUS	fibroblast growth
38	198	17.6	155	1 A60721	acidic fibroblast
39	198	17.6	184	2 S31622	acidic fibroblast
40	197	17.5	155	1 GKBOA	acidic fibroblast
41	196	17.4	152	2 JH0476	acidic fibroblast
42	196	17.4	155	2 JW0055	acidic fibroblast
43	195	17.3	189	2 A48834	basic fibroblast g
44	194.5	17.3	155	1 A40117	basic fibroblast g
45	194	17.2	155	2 A60130	acidic fibroblast

ALIGNMENTS

RESULT 1
I48610
keratinocyte growth factor Fgf-7 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I48610; S33227
R:Wason, I.J.; Fuller-Pace, F.; Smith, R.; Dickson, C.
Mech. Dev. 45, 15-30, 1994
A:Title: FGF-7 (keratinocyte growth factor) expression during mouse development sugge
A:Reference number: I48610; MUID:94242659
A:Accession: I48610
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-194 <RES>
A:Cross-references: EMBL:22703; NID:g297755; PIDN:CAA80403.1; PID:g297756
C:Superfamily: fibroblast growth factor

Query Match 42.8%; Score 481.5; DB 2; Length 194;
Best Local Similarity 47.8%; Pred. No. 3.6e+36;
Matches 99; Conservative 39; Mismatches 54; Indels 15; Gaps 6;
QY 1 MWKWLTHCASAPPHLPGCCCFLLFLVSSVPVTCQALGDMVSPSEATNSSSSSSP 60
Db 1 MRKWILTRILPTLLYR-----SCFHLVCLVGTSLAC-----NDM-SPEQT-ATSYNCSSP 49
QY 61 SSAGRHVSYNHLQ-GDVRWRKLFSTKYFLKIEKNKGVSGTKKENCYPYSILEITSVEIG 119
Db 50 E---RHTRSYDYMGGDIRVRLFCRTQWYLRIDKRGKVGKTQEMKNSYNIIMEITVAVG 106
QY 120 VVAVKAINSNIYLMNKKGLYSGKEFNNDCKLKEIEENGYNTYASFNWHQRMQYVA 179
Db 107 IYVAKGVESEYIYLMNKKGLYAKKEDCNFKELIDENHNTYASAKWTHGGEMFVA 166
QY 180 LNKGAPRGQKTRKNTSAHFLPMVY 206
Db 167 LNKQGIPIVKKTKKEQKTAHFLPNAI 193

RESULT 2
S49501
keratinocyte growth factor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999
C:Accession: S49501
R:Michell, J.E.A.; McInnes, C.J.
submitted to the EMBL Data Library, October 1994
A:Description: Cloning of a cDNA encoding ovine keratinocyte growth factor.
A:Reference number: S49501
A:Accession: S49501
A:Status: preliminary
A:Molecule type: DNA

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RESULT 5
 I50588
 fibroblast growth factor 3 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
 C:Accession: I50588
 R:Mahmood, R.; Kiefer, P.; Guthrie, S.; Dickson, C.; Mason, I.
 Development 121, 1399-1410, 1995
 A:Title: Multiple roles for FGF-3 during cranial neural development in the chicken.
 A:Reference number: I50588; MUID:95309122
 A:Accession: I50588
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-220 <MAH>
 A:Cross-references: EMBL:Z47555; NID:g623215; PIDN:CAA87635.1; PID:g623216
 C:Superfamily: fibroblast growth factor

Query Match 33.2%; Score 374; DB 2; Length 220;
 Best Local Similarity 46.7%; Pred. No. 2.le-26;
 Matches 79; Conservative 30; Mismatches 48; Indels 12; Gaps 2;
 QY 52 SSSSSPSSAGHVRVSYNHLQGDVWRKLFSTFYELKIEKNGKVSCTKENCPSYSL 111
 Db 19 AATASPRAPRDAGRGVGYEHLGAPRRKLYCATYHQLIHPGKINGTLEKNSVFSL 78
 QY 112 EITSVEIGVAVKAINSYLANKKGLYSGKEFNNDCKLKERIEENGYNTYAS--FNW 169
 Db 79 EITAVDVGIVAIKGLFSGRYLANKKGRLYASENYNTECFEVRHELGYNTYASRLYRT 138
 QY 170 QHNG-----ROMYVALNGKAGPRRGOKTRKNTSAHFLPMVHS 208
 Db 139 VPSGASTKKASAEALRWYVYVNGKGPGRGFKTRTQKSSULFPRVDS 187

RESULT 6
 JC4627
 fibroblast growth factor 3 - zebra fish
 C:Species: Brachydanio rerio (zebra fish)
 C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
 C:Accession: JC4627
 R:Kiefer, P.; Straehle, U.; Dickson, C.
 Gene 168, 211-215, 1996
 A:Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic organization
 A:Reference number: JC4627; MUID:96194899
 A:Accession: JC4627
 A:Molecule type: mRNA
 A:Residues: 1-256 <KIE>
 A:Cross-references: EMBL:Z48714; NID:g971333; PIDN:CAA88596.1; PID:g971334
 A:Experimental source: embryo
 A:Note: The authors translated the codon TGG for residue 178 as His
 C:Comment: This factor belongs to the fibroblast growth factor family which have the function is a cell signalling molecule and plays the roles during the early stages of development
 C:Genetics:
 A:Gene: Fgf-3
 A:Introns: 93/2; 127/3
 C:Superfamily: fibroblast growth factor
 C:Keywords: embryo; fibroblast; growth factor

Query Match 33.2%; Score 373; DB 2; Length 256;
 Best Local Similarity 40.8%; Pred. No. 3.le-26;
 Matches 86; Conservative 34; Mismatches 55; Indels 36; Gaps 4;
 QY 25 LLLFLVSVPTQALQDMVSPATNSSSSPSSPSS-----AGHVRVSYNHLQGD 76
 Db 5 LLLLLFLDPSL-----EESLALRLTRAPCARQACDPRQRDAGRGVGYEHLGGA 60
 QY 77 VWRKLFSTFYELKIEKNGKVSCTKENCPSYSLTVEIGVAVKAINSYLANKK 136
 Db 61 PRRKLYCATYHQLIHPGKIDGSLSENNPLSILEITAVDVGIVAIKGLFSGRYLANNE 120

QY 137 KGKLYGSKFNNDDCKLKERIEENGYNTYASFNWONG-----RQ 175
 Db 121 KGRLYASEVFNCEFELEIHELGYNTYAS---RHHTQPPPTGSGIGGSKRRASSKRO 177
 QY 176 MYVALNGKAGPRRGOKTRKNTSAHFLPMV 206
 Db 178 WYVINGKGRPRRGFKTRSTDKASLFLPRVL 208
 RESULT 7
 S39582
 transforming protein int-2 - African clawed frog
 N:Alternate names: FGF-3 protein; fibroblast growth factor 3
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S39582; S25713
 R:Kiefer, P.; Mathieu, M.; Close, M.J.; Peters, G.; Dickson, C.
 EMBO J. 12, 4159-4168, 1993
 A:Title: FGF3 from Xenopus laevis.
 A:Reference number: S39582; MUID:94038898
 A:Accession: S39582
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-237 <KIE>
 A:Cross-references: EMBL:Z25539; NID:g396830; PIDN:CAA80987.1; PID:g396831
 R:Tannahill, D.; Isaacs, H.V.; Close, M.J.; Peters, G.; Slack, J.M.W.
 Development 115, 695-702, 1992
 A:Title: Developmental expression of the Xenopus int-2 (FGF-3) gene: activation by me
 A:Reference number: S25713; MUID:93048831
 A:Accession: S25713
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 39-137 <TAN>
 A:Cross-references: EMBL:X65237; NID:g64855; PIDN:CAA46341.1; PID:g64856
 C:Superfamily: fibroblast growth factor

Query Match 32.1%; Score 361; DB 1; Length 237;
 Best Local Similarity 43.1%; Pred. No. 3.4e-23;
 Matches 85; Conservative 29; Mismatches 67; Indels 16; Gaps 4;
 QY 25 LLLFLVSVPTQALQDMVSPATNSSSSPSSPSS-----SSAGHVRVSYNHLQGDVWRK 81
 Db 7 LLLSTFCGQVQSWAKRLER-EPKYPCSRGKCLDPRQRDAGRGVGYEHLGAPNRK 65
 QY 82 LFSFTKYFLKIEKNGKVSCTKENCPSYSLTVEIGVAVKAINSYLANKKGLY 141
 Db 66 LYCATYHQLIHPGKINGTLEKNSVFSILEITAVDVGIVAIKGLFSGRYLANNGRLY 125
 QY 142 GSKFNNDCKLKERIEENGYNTYAS--FNWONG-----ROMYVALNGKAGPRRG 189
 Db 126 ASETYNPCEFEVRHELGYNTYASRLYRTVPSGAGTKRKASAEALRWYVYVINGKGRPRRG 185
 QY 190 QKTRKNTSAHFLPMV 206
 Db 186 FKTRTQKSSULFPRVL 202
 RESULT 8
 TMST2
 transforming protein (int-2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
 C:Accession: A23930; S08157
 R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.
 EMBO J. 5, 919-924, 1986
 A:Title: Sequence, topography and protein coding potential of mouse-int-2: a putative
 A:Reference number: A23930; MUID:86247582
 A:Accession: A23930
 A:Molecule type: DNA; mRNA
 A:Residues: 1-245 <MOO>
 A:Cross-references: GB:Y00848; GB:M26284; GB:X68450; NID:g52716; PIDN:CAA68767.1; PID
 R:Acland, P.; Dixon, M.; Peters, G.; Dickson, C.

Nature 343, 662-665, 1990
 A:Title: Subcellular fate of the Int-2 oncoprotein is determined by choice of initiation
 A:Reference number: S08157; MUID:90158795

A:Accession: S08157

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 'HSRAGLARGRLVPAPRLRETRAGAAAAGGRCAGM', 3-17 <ACL>

C:Genetics:

A:Gene: int-2

A:Map position: 7

A:Introns: 74/1; 108/3

C:Superfamily: fibroblast growth factor

C:Keywords: growth factor; transforming protein

Query Match 31.4%; Score 353.5; DB 1; Length 245;
 Best Local Similarity 50.0%; Pred. No. 1.7e-24;
 Matches 78; Conservative 22; Mismatches 43; Indels 13; Gaps 3;

QY 63 AGRHVSYNHLOGDVWRKLFSTFYFLKIEKNGKVSQTKKENCPSYLEITSVEIGVVA 122

DB 29 AGGGVYEHLLGAPRRKLYCATYHLQHPGSRVNGS-LENSAYSILEITAVEGVVA 87

QY 123 VKAINSNYLAMNKKGLYKSGKFEFNNDCKLKERIENGNYNYAS--FNWQHNG----- 173

DB 88 IKGLFSRYLAMNKKRGLYASDHYNAECFEVERIHELGYNTYASRLYRTGSSGPGCAORQP 147

QY 174 ---ROMYVALNGKAPRGOKTRRKNTSAHFLPMV 206

DB 148 GAORPMYVSVNGKRPGRGFKTRTKOKSSLFPLRVL 183

RESULT 9
 S04742
 fibroblast growth factor 3 precursor - human
 N:Alternate names: transforming protein int-2
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
 R:Brookes, S.; Smith, R.; Casey, G.; Dickson, C.; Peters, G.
 Oncogene 4, 429-436, 1989
 A:Title: Sequence organization of the human int-2 gene and its expression in teratocarcinoma
 A:Reference number: S04742; MUID:89239468
 A:Accession: S04742
 A:Molecule type: DNA
 A:Residues: 1-239 <BRO>
 A:Cross-references: EMBL:X14445; NID:g33937; PIDN:CAA32615.1; PID:g312409
 C:Genetics:
 A:Gene: GDB:FGF3; INT2
 A:Cross-references: GDB:120103; OMIM:164950
 A:Map position: 11q13.3-11q13.3
 A:Introns: 74/1; 108/3
 C:Superfamily: fibroblast growth factor
 C:Keywords: growth factor
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-239/Product: transforming protein (int-2) #status predicted <MAT>

Query Match 30.4%; Score 342.5; DB 1; Length 239;
 Best Local Similarity 47.4%; Pred. No. 1.6e-23;
 Matches 74; Conservative 26; Mismatches 43; Indels 13; Gaps 2;

QY 63 AGRHVSYNHLOGDVWRKLFSTFYFLKIEKNGKVSQTKKENCPSYLEITSVEIGVVA 122

DB 29 AGGGVYEHLLGAPRRKLYCATYHLQHPGSRVNGS-LENSAYSILEITAVEGVVA 87

QY 123 VKAINSNYLAMNKKGLYKSGKFEFNNDCKLKERIENGNYNYASFNWQ----- 170

DB 88 IRGLFSRYLAMNKKRGLYASDHYNAECFEVERIHELGYNTYASRLYRTGSSGPGCAORQP 147

QY 171 HNGROMYVALNGKAPRGOKTRRKNTSAHFLPMV 206

DB 148 SAERLMTVSVNGKRPGRGFKTRTKOKSSLFPLRVL 183

RESULT 10

S66486

fibroblast growth factor 9 - mouse

A:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S66486

R:Seo, M.; Noguchi, K.

FEBS Lett. 370, 231-235, 1995

A:Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during i

A:Reference number: S66486; MUID:95385801

A:Accession: S66486

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <SEO>

A:Cross-references: EMBL:D38258; NID:gl107458; PIDN:BAA07410.1; PID:gl107459

C:Superfamily: fibroblast growth factor

C:Superfamily: fibroblast growth factor

Query Match 29.2%; Score 328; DB 2; Length 208;

Best Local Similarity 42.8%; Pred. No. 2.8e-22;

Matches 62; Conservative 33; Mismatches 48; Indels 2; Gaps 1;

QY 64 GRHVSYNHLOGDVWRKLFSTFYFLKIEKNGKVSQTKKENCPSYLEITSVEIGVVA 123

DB 48 GPAVTDLHLKLGILRRRLQYCTGFHLEIFPNGTIOGTRKDHRSFGILEFISIAVGLVSI 107

QY 124 KAINSNYLAMNKKGLYKSGKFEFNNDCKLKERIENGNYNTYASFENWQH--NGROMYVALN 181

DB 108 RGVDLSGLYLGMEKELYGSEKLTQECVFRQFEENWNTYSSNLYKHVDTRGRYYVALN 167

QY 182 GKAPRRGOKTRRKNTSAHFLPMV 206

DB 168 KDGTPEGTETRRHQKFTFLPRPV 192

RESULT 11

A48137

fibroblast growth factor 9 - human

N:Alternate names: glia-activating factor

C:Species: Homo sapiens (man)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

R:Matsumoto, M.; Naruo, K.; Seko, C.; Matsumoto, S.; Kondo, T.; Kurokawa, T.

Mol. Cell. Biol. 13, 4251-4259, 1993

A:Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the

A:Reference number: A48137; MUID:93309459

A:Accession: A48137

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-208 <MIY>

A:Cross-references: GB:D14838; NID:g391718; PIDN:BAA03572.1; PID:g391719

A:Experimental source: foreskin

A>Note: sequence extracted from NCBI backbone (NCBIN:134640, NCBI:134641)

C:Genetics:

A:Gene: GDB:FGF9

A:Cross-references: GDB:207221; OMIM:600921

A:Map position: 13q11-13q12

C:Superfamily: fibroblast growth factor

Query Match 29.2%; Score 328; DB 2; Length 208;

Best Local Similarity 42.8%; Pred. No. 2.8e-22;

Matches 62; Conservative 33; Mismatches 48; Indels 2; Gaps 1;

QY 64 GRHVSYNHLOGDVWRKLFSTFYFLKIEKNGKVSQTKKENCPSYLEITSVEIGVVA 123

DB 48 GPAVTDLHLKLGILRRRLQYCTGFHLEIFPNGTIOGTRKDHRSFGILEFISIAVGLVSI 107

QY 124 KAINSNYLAMNKKGLYKSGKFEFNNDCKLKERIENGNYNTYASFENWQH--NGROMYVALN 181

DB 108 RGVDLSGLYLGMEKELYGSEKLTQECVFRQFEENWNTYSSNLYKHVDTRGRYYVALN 167

64 GRHRSYNHLQGDVWRKLFSTFKYFLKIEKNKVGSTKKENCPSYILEITSVEIGVAV 123

Query Match 27.38; Score 307.5; DB 2; Length 208;
 Best Local Similarity 40.18; Pred. No. 2e-20;
 Matches 63; Conservative 36; Mismatches 49; Indels 9; Gaps 2;

QY 52 SSSSFSSPSAGRHVRSYNNHLOGDVRWRKLFSTKYFLKIEKNGKVSQTKKENCYPYSIL 111
 DB 43 SERLSRSAPS-----DLSHLOGILRRRLYCYRTGPHLQILPDGNGVQGTQDHSREGIL 95

QY 112 EITSVEIGVAVKAINSNYLLAMNKKGLYGSKEFNNDCKLKERIEENGYNITYASFNQH 171
 DB 96 EFISVAIGLVSIRGVDYTGILGMDNDKGEFGSEKITSECIFREQFEENWYNTYSSNLYKH 155

QY 172 --NGROMYVALNGCAPRGOKTRKNTSAHFLPNV 206
 DB 156 GDSGRYFVALNKDGTDRDGTFRKRHRKHOKFTHLPRPV 192

Search completed: June 15, 2001, 12:12:40
 Job time: 45 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 15, 2001, 12:11:55 ; Search time 19.72 Seconds

(without alignments)
602.939 Million cell updates/sec

Title: US-09-284-100-2

Perfect score: 1125

Sequence: 1 MNKWLTHCASFPHLPGCC.....GKTRKNTSAHFLPMVVS 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0401.*
- 1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /SID56/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /SID56/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /SID56/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /SID56/gcgdata/geneseq/geneseq/AA1986.DAT.*
 - 8: /SID56/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /SID56/gcgdata/geneseq/geneseq/AA1988.DAT.*
 - 10: /SID56/gcgdata/geneseq/geneseq/AA1989.DAT.*
 - 11: /SID56/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /SID56/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /SID56/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /SID56/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /SID56/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /SID56/gcgdata/geneseq/geneseq/AA1995.DAT.*
 - 17: /SID56/gcgdata/geneseq/geneseq/AA1996.DAT.*
 - 18: /SID56/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /SID56/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /SID56/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1125	100.0	208	18	Human fibroblast g
2	1125	100.0	208	19	Recombinant kerati
3	1125	100.0	208	19	Human keratinocyte
4	1125	100.0	208	19	Keratinocyte growt
5	1125	100.0	208	20	Human keratinocyte
6	1125	100.0	208	20	Human keratinocyte
7	1125	100.0	208	20	Human fibroblast g
8	1125	100.0	208	20	Human FGF-10 prote
9	1125	100.0	208	20	Human fibroblast g
10	1125	100.0	208	21	Human keratinocyte
11	1125	100.0	208	21	Fibroblast growth

12	1125	100.0	208	21	Human keratinocyte
13	1125	100.0	208	21	Human fibroblast g
14	1125	100.0	208	22	Human keratinocyte
15	1125	100.0	243	21	Lung cancer associ
16	1122	99.7	208	19	E.coli optimised K
17	1122	99.7	208	20	E.coli optimised
18	1122	99.7	208	20	Human keratinocyte
19	1122	99.7	208	21	Human KGF-2 E. col
20	1120	99.6	208	19	Human fibroblast g
21	1116	99.2	208	17	Keratinocyte growt
22	1104.5	98.2	206	22	Human KGF-2 deleti
23	1092.5	97.1	209	19	Rat fibroblast gro
24	1088.5	96.8	215	18	E.coli optimised K
25	914	81.2	174	19	E.coli optimised
26	914	81.2	174	20	Truncated E. coli
27	914	81.2	174	20	Human KGF-2 E. col
28	914	81.2	174	21	Human KGF-2 E. col
29	914	81.2	174	21	Human KGF-2 deleti
30	914	81.2	174	21	E.coli optimised K
31	914	81.2	174	21	Human KGF-2 constr
32	909	80.8	184	21	Human KGF-2 mutant
33	909	80.8	184	21	Human hscF10 prote
34	894	79.5	170	19	KGF-2 deletion mut
35	894	79.5	170	22	Human KGF-2 deleti
36	894	79.5	171	19	KGF-2 mutant, KGF2
37	894	79.5	171	20	E.coli optimised K
38	894	79.5	171	21	Human KGF-2 mutant
39	890	79.1	170	19	Human KGF-2 deleti
40	890	79.1	170	19	KGF-2 deletion mut
41	890	79.1	170	19	KGF-2 deletion mut
42	890	79.1	170	19	KGF-2 deletion mut
43	890	79.1	170	19	KGF-2 deletion mut
44	890	79.1	170	19	KGF-2 deletion mut
45	889	79.0	170	19	KGF-2 deletion mut

ALIGNMENTS

RESULT 1	
W24050	
ID	W24050 standard; Protein; 208 AA.
XX	
AC	W24050;
XX	
DT	12-FEB-1998 (first entry)
XX	
DE	Human fibroblast growth factor FGF-10.
XX	
KW	Fibroblast growth factor; rat; human; recombinant DNA; bone disease;
KW	wound healing; cartilage.
XX	
OS	Homo sapiens.
XX	
PN	WO9720929-A1.
XX	
PD	12-JUN-1997.
XX	
PF	06-DEC-1996; 96WO-JP03579.
XX	
PR	24-JUL-1996; 96JP-0214378.
PR	07-DEC-1995; 95JP-0345689.
XX	
PA	28-MAR-1996; 96JP-0103240.
XX	
PI	(SUMU) SUNITOMO PHARM CO LTD.
XX	
DR	Itoh N, Katsumata T, Negoro T, Tagashira S;
XX	
WI	WPI; 1997-319776/29.
DR	N-ESDB; T77200.
XX	
PT	Recombinant fibroblast growth factor FGF-10 and related DNA - useful for the treatment of bone disease and for wound healing

XX PS Claim 1; Page 32-33; 51pp; Japanese.
 XX CC The present sequence represents human fibroblast growth factor FGF-10.
 CC Recombinant FGF-10 DNA, vectors, containing the DNA, and host cells,
 CC containing the vectors, are useful for the recombinant production
 CC of FGF-10. The recombinant FGF-10 is useful for the treatment of
 CC diseases and injury of bone or cartilage, and as a wound healing
 CC promoter.
 XX CC
 XX Sequence 208 AA;

Query Match 100.0%; Score 1125; DB 18; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWKWLTHCASAPPLPGCCGCCFLLLFLVSSVPVTCQALGQDMVSPRATNSSSSSFSSP 60;
 Db 1 mwkwllthcasafphlpgccccfllllflvssvpvtcqlgqdmvspeatnsssfssp 60
 QY 61 SSAGRHVRSYHNLQGDVWRKLFSTFKYFLKIEKNGKVSCTKKENCYPYSILEITSVEIGV 120
 Db 61 ssagrhrvsynhlqgdvwrklfstfkylkieknkgvsgtkkencypysileitsveigv 120
 QY 121 VAVKAINSYYLAMNKKGLYSGKEFNNDCKLKERIEENGYNTYASFNWQHNGRMVVAL 180
 Db 121 vavkainsnyylamnkkglysgkefnndcklkerieengyntyasfnwqhngrmvval 180
 QY 181 NGKGAPRRGQKTRRKNTSAHFLPMVHVS 208
 Db 181 ngkgaprrgqktrrkntsahflpmvhs 208

RESULT 2
 W57264 standard; Protein: 208 AA.
 AC W57264;
 XX 02-SEP-1998 (first entry)
 XX Recombinant keratinocyte growth factor (KGF)-2 protein sequence.
 DE Keratinocyte growth factor-2; KGF-2; variant; human; recombinant;
 KW epithelial cell stimulation; burn; ulcer; inflammatory bowel disease;
 KW lung damage; liver damage; pancreatic disorder; diabetes.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..36
 FT Protein 37..208
 FT /note= "putative leader sequence"
 FT /note= "mature KGF-2"
 XX WO9816642-A1.
 XX 23-APR-1998.
 XX 15-OCT-1997; 97WO-US18607.
 XX 11-DEC-1996; 96US-0033046.
 XX 15-OCT-1996; 96US-0028493.
 XX 06-DEC-1996; 96US-0032781.
 XX (AMGE-) AMGEN INC.
 XX Narhi LO, Osslund TD;
 XX WPI; 1998-251289/22.
 XX N-PSDB; V28937.
 XX

PT New keratinocyte factor-2 variants - used for stimulating epithelial
 PT cells for treating e.g. burns, ulcers, inflammatory bowel disease,
 PT lung damage, liver damage or pancreatic disorders.
 XX Claim 1; Fig 1-1A; 132pp; English.
 PS This represents the recombinant human keratinocyte growth factor
 CC (KGF)-2. The specification provides variants of mature KGF-2 shown in
 CC W57265 to W57271 and W57305 to W57311. A prokaryotic or eukaryotic host
 CC cell containing a vector comprising a polynucleotide encoding the KGF-2
 CC variant operatively linked to an expression control sequence can be used
 CC to produce the variants of KGF-2 by recombinant DNA techniques. The KGF-2
 CC variants and derivatives can be used for the stimulation (including
 CC cytoprotection, proliferation and differentiation), of epithelial cells
 CC including the eye, ear, gums, hair, lung, skin, pancreas (endocrine and
 CC exocrine), thymus, thyroid, urinary bladder, liver and gastrointestinal
 CC tract. They can be used for treating e.g. burns and other partial and
 CC full-thickness injuries in need of stimulation of adnexal structures
 CC such as hair follicles, sweat glands, and sebaceous glands. They are
 CC also useful for the treatment of lesions caused by epidermolysis
 CC bullosa, chemotherapy-induced alopecia and male-pattern baldness,
 CC gastric and duodenal ulcers, gut toxicity, inflammatory bowel diseases
 CC and erosions of the gastrointestinal tract. They are useful in the
 CC treatment of chemotherapy induced pulmonary fibrosis, damage caused by
 CC viral hepatitis, lung injury, gum disease, salivary gland tissue damage,
 CC ear drum damage, autoimmune diseases such as Sjogren's syndrome and
 CC pancreatic disorders including diabetes (type I and type II) and
 CC cystic fibrosis.
 XX Sequence 208 AA;

Query Match 100.0%; Score 1125; DB 19; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWKWLTHCASAPPLPGCCGCCFLLLFLVSSVPVTCQALGQDMVSPRATNSSSSSFSSP 60
 Db 1 mwkwllthcasafphlpgccccfllllflvssvpvtcqlgqdmvspeatnsssfssp 60
 QY 61 SSAGRHVRSYHNLQGDVWRKLFSTFKYFLKIEKNGKVSCTKKENCYPYSILEITSVEIGV 120
 Db 61 ssagrhrvsynhlqgdvwrklfstfkylkieknkgvsgtkkencypysileitsveigv 120
 QY 121 VAVKAINSYYLAMNKKGLYSGKEFNNDCKLKERIEENGYNTYASFNWQHNGRMVVAL 180
 Db 121 vavkainsnyylamnkkglysgkefnndcklkerieengyntyasfnwqhngrmvval 180
 QY 181 NGKGAPRRGQKTRRKNTSAHFLPMVHVS 208
 Db 181 ngkgaprrgqktrrkntsahflpmvhs 208
 RESULT 3
 W59052 standard; Protein: 208 AA.
 ID W59052
 XX W59052;
 AC W59052;
 XX 26-AUG-1998 (first entry)
 XX Human keratinocyte growth factor-2 (KGF-2) protein.
 DE Keratinocyte growth factor-2; KGF-2; epithelial cell production;
 KW hepatitic cirrhosis; fulminant liver failure; gastric ulcer; diabetes;
 KW duodenal ulcer; gut toxicity; inflammatory bowel disease; oesophagitis;
 KW erosive gastritis; oesophageal reflux; gastrointestinal toxicity; human;
 KW pancreatitis; cystic fibrosis; corneal degeneration; gum disease;
 KW urinary bladder damage; ear drum damage; salivary gland damage;
 KW autoimmune disease; Sjogren's Syndrome; sicca syndrome.
 XX Homo sapiens.
 XX

XX 15-JUL-1998 (first entry)
DT Keratinocyte growth factor-2.
XX Keratinocyte growth factor-2; KGF-2; fibroblast growth factor-12; FGF-12;
DE Keratinocyte proliferation; growth stimulator; skin strength; mucositis;
XX Keratinocyte proliferation; wound healing; inflammatory bowel disease; therapy;
KW epidermal thickening; wound healing; inflammatory bowel disease; therapy;
KW inflammation; hair growth promoter.
XX Homo sapiens.
OS WO9806844-A1.
XX 19-FEB-1998.
PD 13-AUG-1997; 97WO-US14112.
XX 28-FEB-1997; 97US-0039045.
PF 13-AUG-1996; 96US-0023852.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Coleman TA, Duan R, Jimenez P, Mendrick D, Moore PA;
PI Ni J, Rampy MA, Ruben SM, Zhang J;
XX WPI; 1998-159536/14.
DR N-PSDB; V19976.
XX Keratinocyte growth factor-2 deletion mutants - useful to promote
PT or accelerate wound healing
XX Claim 1; Fig 1; 25lpp; English.
XX This sequence is the human keratinocyte growth factor-2 (KGF-2). The
CC protein is used to create the mutants of the invention, that stimulate
CC proliferation of keratinocytes. The mutants have enhanced keratinocyte
CC growth stimulating activity as compared to wild-type KGF-2 (also known as
CC fibroblast growth factor-12). They are used to stimulate growth or
CC proliferation of keratinocytes. In particular, they are used to prevent
CC or improve the appearance of wrinkles or aged skin, improving skin
CC strength, promoting epidermal thickening, reducing scarring or improving
CC healing after cosmetic surgery. The mutants are also useful for promoting
CC wound healing, especially where an individual is wound healing impaired.
CC Wounds to be treated may be surgical or excisional wounds, deep wounds
CC involving damage of the dermis and epidermis, eye tissue wounds, dental
CC tissue wounds, oral cavity wounds, diabetic, dermal, cubitus, arterial or
CC venous stasis ulcers or burns. Treatment, especially by anastomosis, of
CC wounds caused by colonic or gastrointestinal surgical procedures can also
CC be achieved through use of the KGF-2 deletion mutants. They can also be
CC used for treatment or prevention of mucositis, inflammatory bowel
CC disease, reduction of inflammation, promoting hair growth, urothelial
CC healing or tissue growth or repair in the female genital tract, or for
CC treating tissue exposed to radiation or protecting tissue to be exposed
CC to radiation (e.g. to allow an increase in radiation dosage used to treat
CC a malignancy).
XX Sequence 208 AA;
SQ

XX 15-JUL-1998 (first entry)
DT Keratinocyte growth factor-2.
XX Keratinocyte growth factor-2; KGF-2; fibroblast growth factor-12; FGF-12;
DE Keratinocyte proliferation; growth stimulator; skin strength; mucositis;
XX Keratinocyte proliferation; wound healing; inflammatory bowel disease; therapy;
KW epidermal thickening; wound healing; inflammatory bowel disease; therapy;
KW inflammation; hair growth promoter.
XX Homo sapiens.
OS WO9806844-A1.
XX 19-FEB-1998.
PD 13-AUG-1997; 97WO-US14112.
XX 28-FEB-1997; 97US-0039045.
PF 13-AUG-1996; 96US-0023852.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Coleman TA, Duan R, Jimenez P, Mendrick D, Moore PA;
PI Ni J, Rampy MA, Ruben SM, Zhang J;
XX WPI; 1998-159536/14.
DR N-PSDB; V19976.
XX Keratinocyte growth factor-2 deletion mutants - useful to promote
PT or accelerate wound healing
XX Claim 1; Fig 1; 25lpp; English.
XX This represents a keratinocyte growth factor-2 (KGF-2) protein. The
CC KGF-2 protein can be used to stimulate the production of epithelial cells
CC selected from cells within the eye, ear, gums, pancreas, urinary bladder,
CC liver and gastrointestinal tract, especially cells in the oral cavity,
CC glandular stomach and small intestine, colon and other cells within the
CC intestinal mucosa. The method comprises contacting the cells with the
CC KGF-2 protein. The KGF-2 proteins can be used to increase cytoprotection,
CC proliferation or differentiation of epithelial cells. They can be used to
CC treat and prevent hepatic cirrhosis, fulminant liver failure, damage
CC caused by acute viral hepatitis, toxic insults to the liver and/or bile
CC duct disorders. They can also be used to treat and prevent gastric
CC ulcers, duodenal ulcers, inflammatory bowel disease, gut toxicity and
CC erosions of the gastrointestinal tract, erosive gastritis, oesophagitis,
CC oesophageal reflux, radiation or chemotherapy induced gastrointestinal
CC toxicity, disorders of the pancreas, e.g. diabetes, pancreatitis or
CC cystic fibrosis, corneal degeneration, gum disease, urinary bladder
CC damage, ear drum damage, salivary gland damage and autoimmune diseases
CC such as Sjogren's Syndrome which can cause salivary gland insufficiency
CC (sicca syndrome).
XX Sequence 208 AA;
SQ

Query Match 100.0%; Score 1125; DB 19; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.3e-112;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWKWLTHCASFPHLPGCCCCFLLFLVSSVPVTCQALGQDMVSPATNSSSSFSFSP 60
DB 1 mwkwilthcasafphlpgcccccflflvssvpvtcqlgqdmvspeatnssssfsfss 60
QY 61 SSAGRHVRSYHNLQGDVWRKLFSTFKYFLKIEKNKVGSGTKKENCPSYILSVEIGV 120
DB 61 ssagrhrvsynhlqgdvwrkrlfstfkyflkieknkvsgtkkencpysileitsveigv 120
QY 121 VAVKAINSYYLAMNKKGLYSGKEFNNDCKLKERTENGNTYASFNWQHNGRMVVAL 180
DB 121 vavkainsnyylamnkglkysgkefnndcklkerieengntynlasfnwqhngqrmvval 180
QY 181 NGKAPRRGKTRKNTSAHFLPMVHVS 208
DB 181 ngkaprrgktrkntsahflpmvhvs 208

RESULT 4
W52581 ID W52581 standard; Protein; 208 AA.
X# AC W52581;

Db 121 vavkainsnyllamkkglyskfndcklkerieengyntasyasfnwqngmryval 180
QY 181 NGKGAPRRGQKTRRKNTSAHFLPMVHVS 208
Db 181 ngkgaprrgqktrrkntsahflpmvhs 208
RESULT 5
ID Y32916 standard; Protein; 208 AA.
XX Y32916;
AC Y32916;
XX Y32916;
DT 03-NOV-1999 (first entry)
XX Human keratinocyte growth factor, KGF-2, protein.
XX Keratinocyte growth factor; KGF-2; human; platelet; fibrinogen; albumin;
KW globulin; total serum protein; blood; hypofibrinogenemia; cirrhosis;
KW disseminated intravascular coagulation; thrombocytopaenia; myelofibrosis;
KW hypalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia;
KW leukaemia; haemolytic syndrome; Zieve's syndrome; rheumatic disease;
KW HELLP preclampsia syndrome; congenital rubella syndrome; systemic lupus;
KW Epstein-Barr infectious mononucleosis; thyrotoxicosis; uraemia; therapy;
KW infection; tissue necrosis; vasculitis; ulcerative bowel disease;
KW serositis; subacute bacterial endocarditis; liver disease; amyloidosis;
KW congestive heart failure; constrictive pericarditis; nephrotic syndrome;
KW cardiac valvular disease; hypoglobulinaemia; keratoconjunctivitis sicca.
XX Homo sapiens.
XX WO9941282-A1.
XX 19-AUG-1999.
XX 12-FEB-1999; 99WO-US03018.
XX 30-DEC-1998; 98US-0114387.
XX 13-FEB-1998; 98US-0074585.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Jimenez P, Louie A, Mendrick D, Rampy MA, Russell D;
XX WPI: 1999-527359/44.
XX N-PSDB; Z11169.
XX Use of keratinocyte growth factor-2 to increase levels of platelets,
XX fibrinogen, albumin, globulin and total serum protein
XX Disclosure; Fig 3; 31pp; English.
XX This sequence represents the human keratinocyte growth factor-2 (KGF-2)
XX protein. Fragments and mutants of this sequence are used in the methods
XX of the invention, for increasing the level of platelets, fibrinogen,
XX albumin, globulin, and total serum protein in the blood. KGF-2 can also
XX be used to stimulate proliferation of salivary gland cells, lacrimal
XX gland cells, sinus epithelium, and Goblet cells. The methods can also be
XX used to treat hypofibrinogenemia caused by a cirrhosis, and disseminated
XX intravascular coagulation (DIC). The methods can be used to treat
XX thrombocytopaenia and to alleviate hypalbuminaemia. These diseases are
XX caused by: drug induced hypersensitivity, thrombocytopaenia purpura,
XX posttransfusion purpura, metastatic tumours in the bone, aplastic
XX anaemia, myelofibrosis, leukaemia, haemolytic syndromes, cancer
XX chemotherapy, Zieve's syndrome, sepsis, HELLP preclampsia syndrome,
XX megaloblastic anaemia peritonitis, congenital rubella syndrome,
XX Epstein-Barr infectious mononucleosis, systemic lupus, preclampsia,
XX thyrotoxicosis, uraemia, rheumatic diseases, granulomatous processes,
XX bacterial viral and parasitic infections, tissue necrosis, vasculitis,
XX ulcerative bowel disease, serositis, subacute bacterial endocarditis,
XX liver disease, amyloidosis, malnutrition, malignancy, congestive heart
XX failure, constrictive pericarditis, cardiac valvular disease, nephrotic

CC syndrome, trauma and crush injuries, gastrointestinal and lymphatic
CC fistulae, and protein-losing gastroenteropathies. The methods can also be
CC used to treat hypoglobulinaemia, total protein loss, damage to the sinus
CC epithelium, and can be used to increase proliferation of epithelial cells
CC of the bladder or prostate, stimulate proliferation of the salivary gland
CC cells and to increase Goblet cell proliferation for treating or
CC preventing keratoconjunctivitis sicca.
XX Sequence 208 AA;
SQ
Query Match 100.0%; Score 1125; DB 20; Length 208;
Best Local Similarity 100.0%; Pred. No. 5.3e-112;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWKWLTHCASFPHLPGCCGCCFLLLFLVSSVPVTCQALGDMVSPATNSSSSSSP 60
Db 1 mwkwilthcasafphlpgcccccflilflvssvptcqlgdmvspeatnsesssfp 60
QY 61 SSAGRHVRSYHNLQDVRWRKLFSTFKYFLKTEKNGKVSQTKKENCPSYILEITSVEIGV 120
Db 61 ssagrhrvrsynhlqgdvrwrklfstfkylkiekngkvsqtkkencpsyleitsvelgv 120
QY 121 VAVKAINSNYLLAMKKGKLYSGKFNNDCKLKERIEENGYNTASYASFNWQHNGRMYVAL 180
Db 121 vavkainsnyllamkkgklyskfndcklkerieengyntasyasfnwqngmryval 180
QY 181 NGKGAPRRGQKTRRKNTSAHFLPMVHVS 208
Db 181 ngkgaprrgqktrrkntsahflpmvhs 208
RESULT 6
Y32888
ID Y32888 standard; Protein; 208 AA.
XX Y32888;
AC Y32888;
XX Y32888;
DT 03-NOV-1999 (first entry)
XX Human keratinocyte growth factor, KGF-2, protein sequence.
XX Keratinocyte growth factor; KGF-2; human; platelet; fibrinogen; albumin;
KW globulin; total serum protein; blood; hypofibrinogenemia; cirrhosis;
KW disseminated intravascular coagulation; thrombocytopaenia; myelofibrosis;
KW hypalbuminaemia; posttransfusion purpura; metastatic tumour; anaemia;
KW leukaemia; haemolytic syndrome; Zieve's syndrome; rheumatic disease;
KW HELLP preclampsia syndrome; congenital rubella syndrome; systemic lupus;
KW Epstein-Barr infectious mononucleosis; thyrotoxicosis; uraemia; therapy;
KW serositis; subacute bacterial endocarditis; liver disease; amyloidosis;
KW congestive heart failure; constrictive pericarditis; nephrotic syndrome;
KW cardiac valvular disease; hypoglobulinaemia; keratoconjunctivitis sicca.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
FT CDS 1..627
FT /*tag= a
FT /product= KGF-2
XX WO9941282-A1.
XX 19-AUG-1999.
XX 12-FEB-1999; 99WO-US03018.
XX 30-DEC-1998; 98US-0114387.
XX 13-FEB-1998; 98US-0074585.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Jimenez P, Louie A, Mendrick D, Rampy MA, Russell D;

XX

DR WPI; 1999-527359/44.
N-PSDB; Z11095.

XX

PT Use of keratinocyte growth factor-2 to increase levels of platelets,
fibrinogen, albumin, globulin and total serum protein

XX

PS Claim 1; Fig 1; 31pp; English.

XX

This sequence is the human keratinocyte growth factor-2 (KGF-2) protein. Fragments and mutants of this sequence are used in the methods of the invention, for increasing the level of platelets, fibrinogen, albumin, globulin, and total serum protein in the blood. KGF-2 can also be used to stimulate proliferation of salivary gland cells, lacrimal gland cells, sinus epithelium, and Goblet cells. The methods can also be used to treat hypofibrinogenemia caused by a cirrhosis and disseminated intravascular coagulation (DIC). The methods can be used to treat thrombocytopenia and to alleviate hypalbuminemia. These diseases are caused by: drug induced hypersensitivity, chromocytopenia purpura, posttransfusion purpura, metastatic tumours in the bone, aplastic anaemia, myelofibrosis, leukaemia, haemolytic syndromes, cancer chemotherapy, Zieve's syndrome, sepsis, HELLIP preclampsia, cancer megaloablastic anaemia peritonitis, congenital rubella syndrome, Epstein-Barr infectious mononucleosis, systemic lupus, preclampsia, chylotoxiosis, uraemia, rheumatic diseases, granulomatous processes, bacterial viral and parasitic infections, tissue necrosis, vasculitis, ulcerative bowel disease, serositis, subacute bacterial endocarditis, liver disease, amyloidosis, malnutrition, malignancy, congestive heart failure, constrictive pericarditis, cardiac valvular disease, nephrotic syndrome, trauma and crush injuries, gastrointestinal and lymphatic fistulae, and protein-losing gastroenteropathies. The methods can also be used to treat hypoglobulinemia, total protein loss, damage to the sinus epithelium, and can be used to increase proliferation of epithelial cells of the bladder or prostate, stimulate proliferation of the salivary gland cells and to increase Goblet cell proliferation for treating or preventing keratoconjunctivitis sicca.

SQ

Sequence 208 AA;

Query Match

Best Local Similarity 100.0%; Score 1125; DB 20; Length 208;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MWKWLTHCASAPHLPGCCCCCLLLFLVSSVPVTCQALGQDMVSPATNSSSSFSFP 60

Db

1 mwkwlthcasafhlpgccccclllflvssvpvtcqlgqdmvspeatnsssfssp 60

QY

61 SSAGRHVRSYNHLOGDVRWKLFSFTKYLKIEKNGKVSCTKENCPCYSILEITSVEIGV 120

Db

61 ssagrhrvrsynhlogdvrvrklfsftkyflkiekngkvsctkencpcysileitsveigv 120

QY

121 VAVKAINSNYYLAMNKGKLYGSKFENNCKLKERIEENGYNTYASFNQHNGRMYYAL 180

Db

121 vavkainsnyylamnkgklygskfenncklkerieengyntyasfnqhngrmymyal 180

QY

181 NGKAPRRGQKTRKNTSAHFLPMVVHS 208

Db

181 ngkagprgqktrkntsahflpmvvhhs 208

RESULT 7

W84564

ID W84564 standard; Protein: 208 AA.

AC

W84564;

XX

31-MAR-1999 (first entry)

XX

Human fibroblast growth factor 10 (FGF-10).

XX

Human; fibroblast growth factor 10; FGF-10; regenerator; activator;

KW

digestive tract tissue; intractable digestive tract lesion;

KW

inflammatory bowel disease; postgastrectomy disturbance;

XX

malabsorption syndrome.

OS

Homo sapiens.

XX

JP10330283-A.

XX

15-DEC-1998.

XX

30-MAY-1997; 97JP-0158079.

XX

30-MAY-1997; 97JP-0158079.

XX

(SUMU) SUMITOMO SEIYAKU KK.

XX

WPI; 1999-135590/12.

DR

N-PSDB; X03346.

XX

New regenerator/activator for digestive tract tissue - useful for

PT

improving intractable digestive tract lesions such as inflammatory

PT

bowel disease, postgastrectomy disturbances and malabsorption

PT

syndrome

XX

Claim 2; Page 5; 7pp; Japanese.

XX

The present sequence represents a human fibroblast growth factor 10

CC

(FGF-10). The protein is used as a regenerator/activator for digestive

CC

tract tissue. The regenerator/activator can improve intractable

CC

digestive tract lesions such as inflammatory bowel disease,

CC

postgastrectomy disturbances and malabsorption syndrome.

CC

Sequence 208 AA;

SQ

Query Match

Best Local Similarity 100.0%; Score 1125; DB 20; Length 208;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MWKWLTHCASAPHLPGCCCCCLLLFLVSSVPVTCQALGQDMVSPATNSSSSFSFP 60

Db

1 mwkwlthcasafhlpgccccclllflvssvpvtcqlgqdmvspeatnsssfssp 60

QY

61 SSAGRHVRSYNHLOGDVRWKLFSFTKYLKIEKNGKVSCTKENCPCYSILEITSVEIGV 120

Db

61 ssagrhrvrsynhlogdvrvrklfsftkyflkiekngkvsctkencpcysileitsveigv 120

QY

121 VAVKAINSNYYLAMNKGKLYGSKFENNCKLKERIEENGYNTYASFNQHNGRMYYAL 180

Db

121 vavkainsnyylamnkgklygskfenncklkerieengyntyasfnqhngrmymyal 180

QY

181 NGKAPRRGQKTRKNTSAHFLPMVVHS 208

Db

181 ngkagprgqktrkntsahflpmvvhhs 208

RESULT 8

W92312

ID W92312 standard; Protein: 208 AA.

XX

W92312;

XX

01-APR-1999 (first entry)

XX

Human FGF-10 protein.

XX

FGF-10; fibroblast growth factor; hypoglycaemia; hyperglycaemia.

XX

Homo sapiens.

XX

JP10330285-A.

XX

15-DEC-1998.

XX

Fri Jun 15 12:17:05 2001

PF 30-MAY-1997; 97JP-0158080.
 XX
 PR 30-MAY-1997; 97JP-0158080.
 XX
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX
 XX WPI; 1999-109362/10.
 DR N-PSDB; X01743.
 XX
 XX New hypoglycaemia agent containing fibroblast growth factor 10 -
 PT useful for improving hyperglycemia
 XX
 PS Claim 2; Page 5-6; 8pp; Japanese.
 XX
 CC This sequence represents a human fibroblast growth factor 10 (FGF-10)
 CC which is used as for improving hypoglycaemia as a novel hypoglycaemia
 CC agent. The hypoglycaemia agent improves hyperglycemia condition gradually
 CC without causing rapid hypoglycaemia.
 CC
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 1125; DB 20; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWKWLTHCASFPHLPGCCGCCCLLLFLVSSVPVTCOALGQDMVSPKATNSSSSSFSFP 60
 DB 1 mwkwilthcasafphlpGCCGCCCLLLflvssvpvtcqlgqdmvspkatsnsssfssp 60
 QY 61 SSAGRHVRSYNHLOGDVRWRKLFSTKYLKIEKNGKVSCTKKENCPSYILEITSVEIGV 120
 DB 61 ssagrhrvrsynhlogdvrrwrlfstkylkiekngkvsctkkencpysileitsveigv 120
 QY 121 VAVKAINSNYYLAMNKGKLYGSKFNNCKLKERIEENGYNTYASFNWONGRQMYVAL 180
 DB 121 vavkainsnyylamnkgklygskfnncklkerieengyntyasfnwongrqmyval 180
 QY 181 NGKGAPRRGQKTRKNTSAHFLPMVWHS 208
 DB 181 ngkgaprrgqktrrkntsaahflpmvwhs 208
 RESULT 9
 W89412
 ID W89412 standard; Protein: 208 AA.
 XX
 AC W89412;
 XX
 DT 09-MAR-1999 (first entry)
 XX
 DE Human fibroblast growth factor 10.
 XX
 KW Human; fibroblast growth factor 10; FGF-10; KGF-2; hepatocyte;
 KW keratinocyte growth factor 2; protection; intractable liver lesion.
 XX
 OS Homo sapiens.
 XX
 FN JF10330284-A.
 XX
 PD 15-DEC-1998.
 XX
 PF 30-MAY-1997; 97JP-0158081.
 XX
 PR 30-MAY-1997; 97JP-0158081.
 XX
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX
 XX WPI; 1999-101000/09.
 DR N-PSDB; W82018.
 XX
 PT New hepatocyte protecting agent - comprises fibroblast growth factor
 PT 10 or keratinocyte growth factor 2

XX Claim 2; Page 5-6; 8pp; Japanese.
 XX
 CC The present invention describes a protecting agent for hepatocytes. The
 CC protecting agent comprises fibroblast growth factor 10 (FGF-10) or
 CC keratinocyte growth factor 2 (KGF-2) as the active component. The
 CC present sequence represents human FGF-10. The protecting agent for
 CC hepatocytes is capable of improving intractable liver lesions.
 CC
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 1125; DB 20; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWKWLTHCASFPHLPGCCGCCCLLLFLVSSVPVTCOALGQDMVSPKATNSSSSSFSFP 60
 DB 1 mwkwilthcasafphlpGCCGCCCLLLflvssvpvtcqlgqdmvspkatsnsssfssp 60
 QY 61 SSAGRHVRSYNHLOGDVRWRKLFSTKYLKIEKNGKVSCTKKENCPSYILEITSVEIGV 120
 DB 61 ssagrhrvrsynhlogdvrrwrlfstkylkiekngkvsctkkencpysileitsveigv 120
 QY 121 VAVKAINSNYYLAMNKGKLYGSKFNNCKLKERIEENGYNTYASFNWONGRQMYVAL 180
 DB 121 vavkainsnyylamnkgklygskfnncklkerieengyntyasfnwongrqmyval 180
 QY 181 NGKGAPRRGQKTRKNTSAHFLPMVWHS 208
 DB 181 ngkgaprrgqktrrkntsaahflpmvwhs 208
 RESULT 10
 B10293
 ID B10293 standard; Protein: 208 AA.
 XX
 AC B10293;
 XX
 DT 20-NOV-2000 (first entry)
 XX
 DE Human keratinocyte growth factor KGF-2 protein SEQ ID NO: 2.
 XX
 KW Human; keratinocyte growth factor; KGF-2; antidiabetic;
 KW antinflammatory; cytoprotective; dermatological; gastrointestinal;
 KW hepatic; respiratory; renal; cerebroprotective; mucositis; treatment;
 KW epithelial cell proliferation; inflammatory bowel disease; lung damage;
 KW liver disorder; diabetes; oral injury; gastrointestinal injury;
 KW gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft;
 KW skin disorder; renal failure; brain injury; intestinal fibrosis;
 KW proctitis; female reproductive tract disorder; pulmonary fibrosis;
 KW pneumonitis; pleural retraction; hemopoietic syndrome; myelotoxicity.
 XX
 OS Homo sapiens.
 XX
 FN Key
 XX
 FH Region
 FT 1..208 /note= "specifically claimed in Claim 276"
 FT 2..208 /note= "specifically claimed in Claim 256"
 FT 36..183 /note= "specifically claimed in Claim 128a"
 FT 36..187 /note= "specifically claimed in Claim 128b"
 FT 36..188 /note= "specifically claimed in Claim 128c"
 FT 36..191 /note= "specifically claimed in Claim 128d"
 FT 36..192 /note= "specifically claimed in Claim 128e"
 FT 36..193 /note= "specifically claimed in Claim 128f"
 FT 36..194 /note= "specifically claimed in Claim 128f"

FT Region /note= "specifically claimed in Claim 128g"
 FT 36..195
 FT /note= "specifically claimed in Claim 128h"
 FT 36..196
 FT /note= "specifically claimed in Claim 128i"
 FT 36..197
 FT /note= "specifically claimed in Claim 128j"
 FT 36..198
 FT /note= "specifically claimed in Claim 128k"
 FT 36..199
 FT /note= "specifically claimed in Claim 128l"
 FT 36..200
 FT /note= "specifically claimed in Claim 128m"
 FT 36..201
 FT /note= "specifically claimed in Claim 128n"
 FT 36..202
 FT /note= "specifically claimed in Claim 128o"
 FT 36..203
 FT /note= "specifically claimed in Claim 128p"
 FT 36..204
 FT /note= "specifically claimed in Claim 128q"
 FT 36..205
 FT /note= "specifically claimed in Claim 128r"
 FT 36..206
 FT /note= "specifically claimed in Claim 128s"
 FT 36..207
 FT /note= "specifically claimed in Claim 128t"
 FT 36..208
 FT /note= "specifically claimed in Claim 128u"
 FT 37..208
 FT /note= "specifically claimed in Claim 128v"
 FT 38..208
 FT /note= "specifically claimed in Claim 128w"
 FT 39..208
 FT /note= "specifically claimed in Claim 128x"
 FT 40..208
 FT /note= "specifically claimed in Claim 128y"
 FT 41..208
 FT /note= "specifically claimed in Claim 128z"
 FT 42..208
 FT /note= "specifically claimed in Claim 129a"
 FT 43..208
 FT /note= "specifically claimed in Claim 129b"
 FT 44..208
 FT /note= "specifically claimed in Claim 129c"
 FT 45..208
 FT /note= "specifically claimed in Claim 129d"
 FT 46..208
 FT /note= "specifically claimed in Claim 129e"
 FT 47..208
 FT /note= "specifically claimed in Claim 129f"
 FT 48..208
 FT /note= "specifically claimed in Claim 129g"
 FT 49..208
 FT /note= "specifically claimed in Claim 129h"
 FT 50..208
 FT /note= "specifically claimed in Claim 129i"
 FT 51..208
 FT /note= "specifically claimed in Claim 129j"
 FT 63..208
 FT /note= "specifically claimed in Claim 129k"
 FT 69..208
 FT /note= "specifically claimed in Claim 129l"
 FT 73..208
 FT /note= "specifically claimed in Claim 129m"
 FT 80..208
 FT /note= "specifically claimed in Claim 129n"
 FT 93..208
 FT /note= "specifically claimed in Claim 129o"
 FT 104..208
 FT /note= "specifically claimed in Claim 129p"
 FT 123..208
 FT /note= "specifically claimed in Claim 129q"

Region 138..208
 /note= "specifically claimed in Claim 4"
 US6077692-A.
 20-JUN-2000.
 13-FEB-1998; 98US-0023082.
 13-AUG-1996; 96US-0023852.
 28-FEB-1997; 97US-0039045.
 13-AUG-1997; 97US-0055561.
 05-JUN-1995; 95US-0461195.
 14-FEB-1995; 95WO-US01790.
 23-MAY-1997; 97US-0862432.
 13-AUG-1997; 97US-0910875.
 (HUMA-) HUMAN GENOME SCI INC.
 Mendrick D, Duan DR, Ni J, Jimenez P, Coleman TA, Gruber JR;
 Dillon PJ, Gentz RL, Ruben SM, Zhang J, Moore PA, Rumpy MA;
 WPI; 2000-441307/38.
 N-PSDB; A71203.
 Novel keratinocyte growth factor useful for promoting and accelerating
 wound healing, comprising at least 10 contiguous amino acids from a
 specific amino acid sequence -
 Claim 1: Fig 1A-C; 190pp; English.
 This invention describes a novel human keratinocyte growth factor, KGF-2
 (I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective,
 dermatological, gastrointestinal, hepatic, respiratory, renal and
 cerebroprotective activity. (I) is useful for stimulating epithelial cell
 proliferation in patients suffering from wound, mucositis, ulcer such as
 venous stasis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful
 for treating inflammatory bowel disease, liver disorder, lung damage,
 diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric
 ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder,
 renal failure, brain injury, breast tissue injury, urothelial damage,
 female reproductive tract disorder, intestinal fibrosis, proctitis,
 pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome
 and myelotoxicity. (I) is also useful for increasing the adherence of
 skin grafts to wound beds and to stimulate re-epithelialization from the
 side effects of gut toxicity, to regenerate skin in full and partial
 thickness skin defects, and to prevent and heal damage to lungs. KGF-2
 shows enhanced activity, increased stability, higher yield and better
 solubility. This sequence represents the human KGF-2 protein described in
 the method of the invention.
 Sequence 208 AA;
 Query Match 100.0%; Score 1125; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWKWLITHCASAFPHLPGCCCCFLILFLVSSVPTVTCQALGQDMVSPKATSSSSSFSSP 60
 Db 1 mwkwilthcasafphlpgcccccflilflvssvptvctqalggdmvspeatnsssfssp 60
 QY 61 SSAGHRVSYNHLQGDVVRWRLKFSFTKFKLIEKNKGVSTKKNCPYSILEITSEVIGV 120
 Db 61 ssaghrvsynhlqgdvvrwrlkfsftkfkyliekngkvgstkkncpysileitsveigv 120
 QY 121 VAVKAINSYLLAMNKKGLYSGKFNNDCKLKERIEENGYNTYASFNWQHNQGMVVAL 180
 Db 121 vavkainsnyllamnkkglysgkfnndcklkerleengyntyasfwnqngmval 180
 QY 181 NGKAPRRGOKTRKNTSAHFLPMVYHS 208
 Db 181 ngkaprrgoktrkntsaahflpmvyhs 208

XX	Sequence	208 AA;
XX	Query Match	100.0%; Score 1125; DB 21; Length 208;
XX	Best Local Similarity	100.0%; Pred. No. 5.3e-112;
XX	Matches 208; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MWKWLTHCASFPHLPGCCCCFLLLFLVSSVPTVCOALQDMVSPKATNSSSSSFSPP 60	
DB	1 mwkwilthcasafphlpgcccccflillflvssvptcgaigdmvspkatsnsssfssp 60	
QY	61 SSAGRHVRYSYNHLQGDVWRKLFSTKYFLKIEKNKGVSGTKKENCPCYSILEITSVEIGV 120	
DB	61 ssagrhrvrsynhlqgdvwrkflsftkyflkieknkgvsgtkkencpcysileitsveigv 120	
QY	121 VAVKALNSNYLLAMNKKGLYGSKEFNNDCKLKERIEENGNTYASFNWQHNGRMVVAL 180	
DB	121 vavkalnsnyllamnkkglygskefnndcklkerieengntyasfnwqhngrmvval 180	
QY	181 NGKGAPRRGQKTRKNTSAHFLPMVVHS 208	
DB	181 ngkgaprrgqktrkntsahflpmvvhs 208	
XX	RESULT 12	
XX	ID B10304 standard; Protein; 208 AA.	
XX	AC B10304;	
XX	DT 20-NOV-2000 (first entry)	
XX	DE Human keratinocyte growth factor KGF-2 protein SEQ ID NO: 24.	
XX	KW Human; keratinocyte growth factor; KGF-2; antiulcer; antidiabetic;	
XX	KW antiinflammatory; cytoprotective; dermatological; gastrointestinal;	
XX	KW hepatic; respiratory; renal; cerebroprotective; mucositis; treatment;	
XX	KW epithelial cell proliferation; inflammatory bowel disease; lung damage;	
XX	KW liver disorder; diabetes; oral injury; gastrointestinal injury;	
XX	KW gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft;	
XX	KW skin disorder; renal failure; brain injury; intestinal fibrosis;	
XX	KW proctitis; female reproductive tract disorder; pulmonary fibrosis;	
XX	KW pneumonitis; pleural retraction; hemopoietic syndrome; myelotoxicity.	
XX	OS Homo sapiens.	
XX	PN US6077692-A.	
XX	PD 20-JUN-2000.	
XX	PF 13-FEB-1998; 98US-0023082.	
XX	PR 13-AUG-1996; 96US-0023852.	
XX	PR 28-FEB-1997; 97US-0039045.	
XX	PR 13-AUG-1997; 97US-0055561.	
XX	PR 05-JUN-1995; 95US-0461195.	
XX	PR 14-FEB-1995; 95WO-US01790.	
XX	PR 23-MAY-1997; 97US-0862432.	
XX	PR 13-AUG-1997; 97US-0910875.	
XX	PA (HUMA-) HUMAN GENOME SCI INC.	
XX	PI Mendrick D, Duan DR, Ni J, Jimenez P, Coleman TA, Gruber JR;	
XX	PI Dillon PJ, Gentz RL, Ruben SM, Zhang J, Moore PA, Rumpy MA;	
XX	WPI; 2000-441307/38.	
XX	Novel keratinocyte growth factor useful for promoting and accelerating	
XX	wound healing, comprising at least 10 contiguous amino acids from a	
XX	specific amino acid sequence	
XX	Disclosure: Fig 2A-C; 190pp; English.	
XX	This invention describes a novel human keratinocyte growth factor, KGF-2,	
XX	(I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective,	
XX	dermatological, gastrointestinal, hepatic, respiratory, renal and	
XX	cerebroprotective activity. (I) is useful for stimulating epithelial cell	
XX	proliferation in patients suffering from wound, mucositis, ulcer such as	
XX	venous stasis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful	
XX	for treating inflammatory bowel disease, liver disorder, lung damage,	
XX	diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric	
XX	ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder,	
XX	renal failure, brain injury, breast tissue injury, urothelial damage,	
XX	female reproductive tract disorder, intestinal fibrosis, proctitis,	
XX	pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome	
XX	and myelotoxicity. (I) is also useful for increasing the adherence of	
XX	skin grafts to wound beds and to stimulate re-epithelialization from the	
XX	wound bed, to produce changes in hepatocyte proliferation, to reduce the	
XX	side effects of gut toxicity, to regenerate skin in full and partial	
XX	thickness skin defects, and to prevent and heal damage to lungs. KGF-2	
XX	shows enhanced activity, increased stability, higher yield and better	
XX	solubility. This sequence represents the fibroblast growth factor KGF2	

PS Disclosure: Fig 3A-D; 190pp; English.

XX This invention describes a novel human keratinocyte growth factor, KGF-2
 CC (I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective,
 CC dermatological, gastrointestinal, hepatic, respiratory, renal and
 CC cerebroprotective activity. (I) is useful for stimulating epithelial cell
 CC proliferation in patients suffering from wound, mucositis, ulcer such as
 CC venous stasis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful
 CC for treating inflammatory bowel disease, liver disorder, lung damage,
 CC diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric
 CC ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder,
 CC renal failure, brain injury, breast tissue injury, urothelial damage,
 CC female reproductive tract disorder, intestinal fibrosis, proctitis,
 CC pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome
 CC and myelotoxicity. (I) is also useful for increasing the adherence of
 CC skin grafts to wound beds and to stimulate re-epithelialization from the
 CC wound bed, to produce changes in hepatocyte proliferation, to reduce the
 CC side effects of gut toxicity, to regenerate skin in full and partial
 CC thickness skin defects, and to prevent and heal damage to lungs. KGF-2
 CC shows enhanced activity, increased stability, higher yield and better
 CC solubility. This sequence represents the human KGF-2 protein described in
 CC the method of the invention.

XX Sequence 208 AA;

Query Match 100.0%; Score 1125; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWKWLTHCASFPHLPGCCCCFLFLVSVVPTCOALGDMVSPATNSSSSSFSSP 60.
 DB 1 mwkwilthcassaafhlpgccccflflvsvvptcqlgqdmvspatnsssssfssp 60.
 QY 61 SSAGRHVRSYHLOGDVRWRKLFSTFKYFLKIEKNGKVSCTKENCPSYILEITSVEIGV 120
 DB 61 ssagrhvrsynhlogdvrrwrkflstfkyflkiekngkvsctkencpysileitsveigv 120
 QY 121 VAVKAINSYYLAMNKKGLYSGKEFNNDCKLKERIEENGYNTYASFNWOHNGRMVVAL 180
 DB 121 vavkainsnyylamnkkglysgkefnndcklkerieengyntasyfnwqhngrmvval 180
 QY 181 NGKGAPRRGOKTRRKNNTSAHFLPMVHVS 208
 DB 181 ngkgaprrgqktrrknntsahflpmvvhvs 208

RESULT 13
 Y70688
 ID Y70688 standard; Protein; 208 AA.
 AC Y70688;
 XX
 DT 18-JUL-2000 (first entry)
 DE Human fibroblast growth factor-10 (fgf).
 KW Fibroblast growth factor; fgf-10; human; growth modulator; hedgehog; hh;
 KW patched; ptc; lung; therapeutic agent; antiproliferative; anticancer;
 KW vulnary; antirheumatic; hypotensive; anti-inflammatory; antiasthmatic;
 KW antiarthritic; tuberculostatic; antimicrobial; antiallergy; bronchitis;
 KW treatment; prevention; lung diseases; cystic fibrosis; asthma; cancer;
 KW emphysema; respiratory distress syndrome; tuberculosis; wound healing;
 KW lung transplantation.

OS Homo sapiens.
 XX
 PN W0200015246-A2.
 XX
 PD 23-MAR-2000.
 XX
 PF 10-SEP-1999; 99WO-US20500.
 XX

PR 11-SEP-1998; 98US-0099952.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Pepicelli C, Lewis P, McMahon AP;
 XX
 DR WPI; 2000-271252/23.
 DR N-PSDB; Z52267.

Modulation of lung tissue or cell growth rate used for treating or
 preventing damage to lung tissue comprises ectopically contacting
 tissue with hedgehog therapeutic, patched therapeutic or fibroblast
 growth factor-10

Disclosure; Page 143; 143pp; English.

The patent discloses a method for modulating the growth state of
 epithelial or mesenchymal cells of the lung, by ectopically contacting
 the tissue with a therapeutic agent, that can effectively alter the rate
 of proliferation of cells. This agent can be selected from hedgehog (hh),
 patched (ptc) or fibroblast growth factor (fgf)-10 therapeutics. It
 involves a direct or indirect antagonism of patched-mediated regulation
 of gene expression. This method is useful for the treatment or prevention
 of lung diseases, like cancer, cystic fibrosis, bronchopneumoconiosis,
 bronchitis, bronchospasm, sarcoidosis, silicosis, eosinophilic granuloma,
 ankylosing spondylitis, emphysema, tuberculosis, respiratory distress
 syndrome, allergic rhinitis, asthma, pulmonary fibrosis and primary
 pulmonary hypertension. It is also used to control wound healing or other
 reformation processes in the lung and augment lung transplantation. The
 present sequence is the human fibroblast growth factor-10 (fgf). It is
 an important component of the hedgehog regulatory network present in
 the embryonic lung, that controls proliferation, pattern formation
 and differentiation.

XX Sequence 208 AA;

Query Match 100.0%; Score 1125; DB 21; Length 208;
 Best Local Similarity 100.0%; Pred. No. 5.3e-112;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWKWLTHCASFPHLPGCCCCFLFLVSVVPTCOALGDMVSPATNSSSSSFSSP 60
 DB 1 mwkwilthcassaafhlpgccccflflvsvvptcqlgqdmvspatnsssssfssp 60
 QY 61 SSAGRHVRSYHLOGDVRWRKLFSTFKYFLKIEKNGKVSCTKENCPSYILEITSVEIGV 120
 DB 61 ssagrhvrsynhlogdvrrwrkflstfkyflkiekngkvsctkencpysileitsveigv 120
 QY 121 VAVKAINSYYLAMNKKGLYSGKEFNNDCKLKERIEENGYNTYASFNWOHNGRMVVAL 180
 DB 121 vavkainsnyylamnkkglysgkefnndcklkerieengyntasyfnwqhngrmvval 180
 QY 181 NGKGAPRRGOKTRRKNNTSAHFLPMVHVS 208
 DB 181 ngkgaprrgqktrrknntsahflpmvvhvs 208

RESULT 14
 B60201
 ID B60201 standard; Protein; 208 AA.
 XX
 AC B60201;
 XX
 DT 27-MAR-2001 (first entry)
 DE Human keratinocyte growth factor-2 (KGF-2), SEQ ID NO:2.
 KW Human; keratinocyte growth factor-2; KGF-2; wound healing; vulnary;
 KW epithelial cell proliferation; epidermal keratinocyte proliferation;
 KW soft tissue growth; ischaemic injury; skin disorder;
 KW skin graft adherence.

OS Homo sapiens.
XX WO200072872-A1.
XX 07-DEC-2000.
XX 02-JUN-2000; 2000WO-US15186.
XX 02-JUN-1999; 99US-0137448.
XX 22-OCT-1999; 99US-0160913.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (GENTZ/) GENTZ R L.
XX (CHOP/) CHOPRA A.
XX (KAUS/) KAUSHAL P.
XX (SPIT/) SPITZNAGEL T.
XX (UNSW/) UNSWORTH E.
XX (KHAN/) KHAN F.
XX Gentz RL, Chopra A, Kaushal P, Spitznagel T, Unsworth E, Khan F;
PI WPI: 2001-041105/05.
XX N-PSDB; C92931.
XX Pharmaceutical composition useful for stimulating epithelial cell
XX proliferation and basal keratinocytes for wound healing comprises
XX keratinocyte growth factor-2, in liquid or lyophilized forms -
XX Disclosure; Fig 1A-C; 101pp; English.
XX The invention relates to a pharmaceutical composition comprising
XX 0.02-40 mg/ml (w/v) keratinocyte growth factor-2 (KGF-2) protein; a
XX buffer having buffering capacity of pH 5-8 at 5-50 mM; a diluent to bring
XX the composition to a designated volume; and a preservative such as
XX m-cresol, chlorobutanol, or a mixture of methyl paraben and propyl
XX paraben or their reaction products. The KGF-2 used in the composition of
XX the invention is preferably a novel mutant selected from the KGF-2
XX deletion mutants B60202 and B60204-B60214, and particularly the deletion
XX mutant KGF-2 delta-33 (B60202). KGF-2 stimulates the proliferation of
XX epithelial cells and epidermal keratinocytes but not mesenchymal cells
XX such as fibroblasts. The compositions of the invention may therefore be
XX used for promoting or accelerating soft tissue growth or wound healing,
XX or for treating mucocystis or inflammatory bowel disease. The compositions
XX may be used to promote the healing of both superficial and deep wounds,
XX in individuals with normal wound healing capacity, and in those in whom
XX healing is impaired (e.g., those with conditions, and ischaemic blockage or
XX infection, immunosuppression, malnutrition, and ischaemic blockage or
XX injury). The compositions may also be used to stimulate the healing of
XX eye tissue wounds, dental tissue wounds, oral cavity wounds, vascular
XX and dermal ulcers, burns, wounds associated with ischaemic injury,
XX and skin disorders such as psoriasis and epidermolysis bullosa. The KGF-2
XX compositions may additionally be used to increase the adherence of skin
XX grafts to a wound bed, to stimulate re-epithelialisation from the wound
XX bed, and to reduce the side effects of gut toxicity that result from
XX radiation, chemotherapy treatments or viral infections. The compositions
XX of the invention are stable over prolonged periods of storage, have
XX increased KGF-2 pharmacological activity and/or facilitate the
XX application or administration of KGF-2 in therapeutic regimens. The
XX present sequence represents human KGF-2.
XX Sequence 208 AA;

Query Match 100.0%; Score 1125; DB 22; Length 208;
Best Local Similarity 100.0%; Pred. No. 5,3e-112;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWKWLTHCASFHPLPGCCCCFLLLFVSSVPVTCQALGQDMVSPFATNSSSSSFSSP 60
DB 1 mwkwlthcasafhplpgccccflillfvlssvpvtcqlgqdmvspfatnsssssfssp 60
QY 61 SSAGRHVRSYHNLQGDVWRKLFSTFKYFLKIEKNGKVSCTKKENCPCYSILEITSVEIGV 120

DB 61 ssagrhvrsynhlqgdvwrklfstfkylkiekngkvsctkkencpcysileitsveigv 120
QY 121 VAVKALNSNYLAMNKKGLYSGKEFNNDCKLKERIEENGYNITYASFNNQHNCRMYVAL 180
DB 121 vavkainsnyylamnkkgklysgkefnndcklkerieengynityasfnwqhgqrmyval 180
QY 181 NGKAPRSGQKTRKNTSAHFLPMVHVS 208
DB 181 ngkgaprrgqktrrkntsaahflpmvhs 208
RESULT 15
B58248
ID B58248 standard; Protein; 243 AA.
XX B58248;
XX 14-MAR-2001 (first entry)
XX Lung cancer associated polypeptide sequence SEQ ID 586.
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
XX cardioactive; immunomodulatory; muscular active; vulnerary;
XX gastrointestinal; nephrotropic; antiinfective; gynecological;
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
XX proliferative disorder; wound healing; infectious disease.
XX Homo sapiens.
XX WO200055180-A2.
XX 21-SEP-2000.
XX 08-MAR-2000; 2000WO-US05918.
XX 12-MAR-1999; 99US-0124270.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.
XX Ruben SM;
XX WPI: 2000-587514/55.
XX N-PSDB; F18124.
XX Lung cancer associated gene sequences, referred to as lung cancer
XX antigens, useful for treatment, prevention, and diagnosis of disorders
XX such as lung cancer -
XX Claim 11; Page 1079-1080; 1425pp; English.
XX Polynucleotide sequences F17982 - F18424 encode human lung cancer
XX associated proteins represented in F58106 - B58548. Lung cancer
XX associated proteins and polynucleotide sequences, their agonists, and
XX antagonists may have neuroprotective; cytostatic; cardioactive;
XX immunomodulatory; muscular active general; vulnerary; gastrointestinal
XX general; nephrotropic; antiinfective; gynecological; of antibacterial
XX activity. The invention also includes antibodies specific for the protein
XX or polynucleotide sequences. The lung cancer associated polynucleotide
XX sequences may be used for detection of lung cancer, chromosome
XX identification, as chromosome markers, and for numerous other diagnostic
XX or research purposes. The proteins may be used to treat disorders such as
XX neurovascular, renal, and proliferative disorders. The proteins may also
XX be used in the treatment of wounds and infectious diseases
XX Polynucleotide sequences F18425 - F18433 and peptide B58549 are used in
XX the course of the invention for the identification and characterisation
XX of the polynucleotide and protein sequences.
XX Sequence 243 AA;

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Query Match      100.0%; Score 1125; DB 21; Length 243;
Best Local Similarity 100.0%; Pred. NO. 6.6e-112;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWKWLTHCASFPHLPGCCGCCFLLFLVSSVPVTCQALGQDMVSPDATNSSSSSFSSP 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 36 mwkwllthcasafphlp9cccccflflfvsrvptcqaigqdmvspeatnsssfssp 95
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SSAGRHRVRSYNNHLOGDVWRKLFSTKYFLKIEKNGKVSQTKKENCPCYSILEITSVEIGV 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 96 ssagrhrvrsyahlqgdvwrklfsftkyflkiekngkvsqtkkencpcysileitsveigv 155
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 VAVKAINSYYIAMNKKKLYGSKFNFNDCKLKERIEENCYNTYASFNWOHNGROMYVAL 180
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 156 vavkainsyyiamnkkklygskfndcklkerieengyntyasfnwqhngrgmyval 215
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 NGKGAPRRGQKTRRKNTSAHFLPMVHVS 208
   |||||||||||||||||||||||||||||||
Db 216 ngkgaprrgqktrrkntsahflpmvhs 243
   |||||||||||||||||||

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